(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
28 February 2002 (28.02.2002)

PCT

(10) International Publication Number
WO 02/16649 A2

(51) International Patent Classification[7]: C12Q 1/68

(21) International Application Number: PCT/US01/26519

(22) International Filing Date: 27 August 2001 (27.08.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/227,948 25 August 2000 (25.08.2000) US
60/228,854 29 August 2000 (29.08.2000) US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/16649 A2

(54) Title: PROBES AND DECODER OLIGONUCLEOTIDES

(57) Abstract: The present invention is directed to improved methods and compositions for the use of adapter sequences on arrays in a variety of multiplexed nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

PROBES AND DECODER OLIGONUCLEOTIDES

This application claims the benefit of U.S.S.N.s 60/227,948 filed August 25, 2000 and 60/228,854, filed August 29, 2001, both of which are expressly incorporated herein by reference.

FIELD OF THE INVENTION

The present invention is directed to methods and compositions for the use of adapter sequences on arrays in a variety of nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

BACKGROUND OF THE INVENTION

The detection of specific nucleic acids is an important tool for diagnostic medicine and molecular biology research. Gene probe assays currently play roles in identifying infectious organisms such as bacteria and viruses, in probing the expression of normal and mutant genes and identifying mutant genes such as oncogenes, in typing tissue for compatibility preceding tissue transplantation, in matching tissue or blood samples for forensic medicine, and for exploring homology among genes from different species.

Ideally, a gene probe assay should be sensitive, specific and easily automatable (for a review, see Nickerson, Current Opinion in Biotechnology 4:48-51 (1993)). The requirement for sensitivity (i.e. low detection limits) has been greatly alleviated by the development of the polymerase chain reaction (PCR) and other amplification technologies which allow researchers to amplify exponentially a specific nucleic acid sequence before analysis (for a review, see Abramson et al., Current Opinion in Biotechnology, 4:41-47 (1993)).

Specificity, in contrast, remains a problem in many currently available gene probe assays. The extent of molecular complementarity between probe and target defines the specificity of the interaction. Variations in the concentrations of probes, of targets and of salts in the hybridization medium, in the reaction temperature, and in the length of the probe may alter or influence the specificity of the

probe/target interaction.

It may be possible under some circumstances to distinguish targets with perfect complementarity from targets with mismatches, although this is generally very difficult using traditional technology, since small variations in the reaction conditions will alter the hybridization. New experimental techniques for mismatch detection with standard probes include DNA ligation assays where single point mismatches prevent ligation and probe digestion assays in which mismatches create sites for probe cleavage.

Recent focus has been on the analysis of the relationship between genetic variation and phenotype by making use of polymorphic DNA markers. Previous work utilized short tandem repeats (STRs) as polymorphic positional markers; however, recent focus is on the use of single nucleotide polymorphisms (SNPs), which occur at an average frequency of more than 1 per kilobase in human genomic DNA. Some SNPs, particularly those in and around coding sequences, are likely to be the direct cause of therapeutically relevant phenotypic variants and/or disease predisposition. There are a number of well known polymorphisms that cause clinically important phenotypes; for example, the apoE2/3/4 variants are associated with different relative risk of Alzheimer's and other diseases (see Cordor et al., Science 261(1993). Multiplex PCR amplification of SNP loci with subsequent hybridization to oligonucleotide arrays has been shown to be an accurate and reliable method of simultaneously genotyping at least hundreds of SNPs; see Wang et al., Science, 280:1077 (1998); see also Schafer et al., Nature Biotechnology 16:33-39 (1998). The compositions of the present invention may easily be substituted for the arrays of the prior art.

There are a variety of particular techniques that are used to detect sequence, including mutations and SNPs. These include, but are not limited to, ligation based assays, cleavage based assays (mismatch and invasive cleavage such as Invader™), single base extension methods (see WO 92/15712, EP 0 371 437 B1, EP 0317 074 B1; Pastinen et al., Genome Res. 7:606-614 (1997); Syvänen, Clinica Chimica Acta 226:225-236 (1994); and WO 91/13075), and competitive probe analysis (e.g. competitive sequencing by hybridization; see below).

Oligonucleotide ligation amplification ("OLA", which is referred as the ligation chain reaction (LCR) when two-stranded reactions or nested reactions are done) involves the ligation of two smaller probes into a single long probe, using the target sequence as the template. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; WO 97/31256 and WO 89/09835, all of which are incorporated by reference.

Invasive cleavage technology is based on structure-specific nucleases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with a non-complementary overlap. The enzyme cleaves at the overlap due to its recognition of the "tail", and releases the "tail" with a label. This can then be

detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.

An additional technique utilizes sequencing by hybridization. For example, sequencing by hybridization has been described (Drmanac et al., Genomics 4:114 (1989); Koster et al., Nature Biotechnology 14:1123 (1996); U.S. Patent Nos. 5,525,464; 5,202,231 and 5,695,940, among others, all of which are hereby expressly incorporated by reference in their entirety).

Sensitivity, i.e. detection limits, remain a significant obstacle in nucleic acid detection systems, and a variety of techniques have been developed to address this issue. Briefly, these techniques can be classified as either target amplification or signal amplification. Target amplification involves the amplification (i.e. replication) of the target sequence to be detected, resulting in a significant increase in the number of target molecules. Target amplification strategies include the polymerase chain reaction (PCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

Alternatively, rather than amplify the target, alternate techniques use the target as a template to replicate a signalling probe, allowing a small number of target molecules to result in a large number of signalling probes, that then can be detected. Signal amplification strategies include the ligase chain reaction (LCR), cycling probe technology (CPT), invasive cleavage techniques such as Invader™ technology, Q-Beta replicase (QβR) technology, and the use of "amplification probes" such as "branched DNA" that result in multiple label probes binding to a single target sequence.

The polymerase chain reaction (PCR) is widely used and described, and involves the use of primer extension combined with thermal cycling to amplify a target sequence; see U.S. Patent Nos. 4,683,195 and 4,683,202, and PCR Essential Data, J. W. Wiley & sons, Ed. C.R. Newton, 1995, all of which are incorporated by reference. In addition, there are a number of variations of PCR which also find use in the invention, including "quantitative competitive PCR" or "QC-PCR", "arbitrarily primed PCR" or "AP-PCR", "immuno-PCR", "Alu-PCR", "PCR single strand conformational polymorphism" or "PCR-SSCP", allelic PCR (see Newton et al. Nucl. Acid Res. 17:2503 91989); "reverse transcriptase PCR" or "RT-PCR", "biotin capture PCR", "vectorette PCR". "panhandle PCR", and "PCR select cDNA subtraction", among others.

Strand displacement amplification (SDA) is generally described in Walker et al., in Molecular Methods for Virus Detection, Academic Press, Inc., 1995, and U.S. Patent Nos. 5,455,166 and 5,130,238, all of which are hereby incorporated by reference.

Nucleic acid sequence based amplification (NASBA) is generally described in U.S. Patent No. 5,409,818 and "Profiting from Gene-based Diagnostics", CTB International Publishing Inc., N.J., 1996,

both of which are incorporated by reference.

Cycling probe technology (CPT) is a nucleic acid detection system based on signal or probe amplification rather than target amplification, such as is done in polymerase chain reactions (PCR). Cycling probe technology relies on a molar excess of labeled probe which contains a scissile linkage of RNA. Upon hybridization of the probe to the target, the resulting hybrid contains a portion of RNA:DNA. This area of RNA:DNA duplex is recognized by RNAseH and the RNA is excised, resulting in cleavage of the probe. The probe now consists of two smaller sequences which may be released, thus leaving the target intact for repeated rounds of the reaction. The unreacted probe is removed and the label is then detected. CPT is generally described in U.S. Patent Nos. 5,011,769, 5,403,711, 5,660,988, and 4,876,187, and PCT published applications WO 95/05480, WO 95/1416, and WO 95/00667, all of which are specifically incorporated herein by reference.

The oligonucleotide ligation assay (OLA) involve the ligation of at least two smaller probes into a single long probe, using the target sequence as the template for the ligase. See generally U.S. Patent Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; and WO 89/09835, all of which are incorporated by reference.

Invader™ technology is based on structure-specific polymerases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with overlap. For mismatch discrimination, the invader technology relies on complementarity at the overlap position where cleavage occurs. The enzyme cleaves at the overlap, and releases the "tail" which may or may not be labeled. This can then be detected. The Invader™ technology is described in U.S. Patent Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.

"Branched DNA" signal amplification relies on the synthesis of branched nucleic acids, containing a multiplicity of nucleic acid "arms" that function to increase the amount of label that can be put onto one probe. This technology is generally described in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference.

Similarily, dendrimers of nucleic acids serve to vastly increase the amount of label that can be added to a single molecule, using a similar idea but different compositions. This technology is as described in U.S. Patent No. 5,175,270 and Nilsen et al., J. Theor. Biol. 187:273 (1997), both of which are incorporated herein by reference.

U.S.S.N.s 09/189,543; 08/944,850; 09/033,462; 09/287,573; 09/151,877; 09/187,289 and 09/256,943; and PCT applications US98/09163 and US99/14387; US98/21193; US99/04473 and US98/05025, all

of which are expressly incorporated by reference, describe novel compositions utilizing substrates with microsphere arrays, which allow for novel detection methods of nucleic acid hybridization.

The use of adapter-type sequences that allow the use of universal arrays has been described in limited contexts; see for example Chee et al., Nucl. Acid Res. 19:3301 (1991); Shoemaker et al., Nature Genetics 14:450 (1996); U.S. Patent Nos. 5,494,810, 5,830,711, 6,027,889, 6,054,564, and 6,268,148; and EP 0 799 897 A1; WO 97/31256, all of which are expressly incorporated by reference.

Accordingly, it is an object of the present invention to provide methods for detecting nucleic acid reactions, and other target analytes, on arrays using adapter sequences.

SUMMARY OF THE INVENTION

In accordance with the above objects, the invention also provides a method of detecting a target nucleic acid. The method comprises contacting the target nucleic acid with an adapter sequence such that the target nucleic acid is joined to the adapter sequence to form a modified target nucleic acid. In addition, the method comprises contacting the modified target nucleic acid with an array comprising a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified target nucleic acid form a complex, wherein the microspheres are distributed on the surface, and detecting the presence fo the target nucleic acid. In addition the method comprises adding at least one decoding binding ligand to the array such that the identity of the target nucleic acid is determined. Preferably the adapter nucleic acids include a sequence as set forth in Table Table I, Table II, Table III or Table IV.

In addition the invention provides a method of making an array. The method comprises forming a surface comprising individual sites on a substrate, distributing microspheres on the surface such that the individual sites contain microspheres, wherein the microspheres comprise at least a first and a second subpopulation each comprising a capture probe, wherein the capture probe is complementary to an adapter sequence, the adapter sequence joined to a target nucleic acid, and an identifier binding ligand that will bind at least one decoder binding ligand such that the identification of the target nucleic acid is elucidated. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

In addition the invention provides a kit comprising at least one nucleic acid selected from the group consisting of the sequences set forth it Table I, Table II, Table III or Table IV. In one embodiment the invention provides a kit that includes a nucleic acid that includes a sequence as set forth in Table I, Table II, Table III or Table IV and at least a first universal priming sequence.

In addition the invention includes an array composition comprising a first population of microspheres comprising first and second subpopulations, wherein the first subpopulation includes a first nucleic acid selected from the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the invention includes an array composition comprising a first sequence at a known location on a substrate, wherein the first sequence is selected from the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the invention includes a method for making an array. The method includes distributing a population of microspheres on an substrate, wherein the population includes first and second subpopulations, wherein the first subpopulation includes a first sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV.

In addition the method includes a method of immobilizing a target nucleic acid. The method includes hybridizing a first adapter probe with a first target nucleic acid, wherein the first adapter probe comprises a first domain that is complementary to the first target nucleic acid and a second domain, comprising a first sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV to form a first hybridization complex. In addition the method includes contacting the first hybridization complex with a first capture probe immobilized on a first substrate, wherein the first capture probe is substantially complementary to the second domain of the first adapter probe.

In addition the invention includes a method of decoding an array composition comprising providing an array composition that includes a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on the surface. The method further includes adding a plurality of decoding binding ligands to the array composition to identify the location of at least a plurality of the bioactive agents wherein at least a first decoder binding ligand comprises a sequence selected from the group consisting of the sequences of Table I, Table II, Table III or Table IV.

A method of detecting a target nucleic acid sequence, said method comprising attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein the first adapter nucleic acid includes a sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV. The method further includes contacting the modified first target nucleic acid sequence with an array comprising a substrate with a patterned surface

comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified first target nucleic acid sequence form a hybridization complex; wherein the microspheres are distributed on the surface and detecting the presence of the modified first target nucleic acid sequence.

DETAILED DESCRIPTION OF THE FIGURES

Figure 1 depicts a method of selecting oligonucleotide sequences.

Figure 2 depicts a scheme for selection of probes and decoder oligonucleotides.

Figure 3 demonstrates hybridization intensity comparison of immobilized beads using non-purified oligonucleotides with HPLC purified oligonucleotides.

Figure 4 depicts different oligonucleotide sequences immobilized onto silica beads at various salt concentration. Average intensity indicates hybridization intensity of beads in a BeadArray.

Figure 5 depicts immobilization of oligonucleotides in increasing salt concentrations.

DETAILED DESCRIPTION OF THE INVENTION

This invention is directed to the use of adapter sequences, and optionally capture extender probes, that allow the use of "universal" arrays. That is, a "universal" array is an array with a set of capture probes that will hybridize to adapter sequences, for use in any number of different reactions, including the binding of nucleic acid reactions and other target analytes comprising a nucleic acid adapter sequence that can hybridize to the array. In this way, a manufacturer of arrays can make one type of array that may be used in a variety of applications, thus reducing the manufacturing costs associated with the array. In addition, in the case of bead arrays, the decoding steps as outlined below can be simplified, as one set of decoding probes can be made.

In general, the use of adapter sequences can be described as follows for nucleic acid reactions. An adapter sequence can be added exogenously to a target nucleic acid sequence using any number of different techniques, including, but not limited to, amplification reactions as described in U.S.S.N. 09/425,633, filed October 22, 1999; 09/513,362, filed February 25, 2000; 09/517,945, filed March 3, 2000; 09/535,854, filed March 27, 2000; 09/553,993, filed April 20, 2000; 09/556,463, filed April 21, 2000; 60/135,051, filed May 20, 1999; 60/135,053, filed May 20, 1999; 60/135,123, filed May 20, 1999; 60/130,089, filed April 20, 1999; 60/160,917, filed October 22, 1999; 60/160,927, filed October 22,

1999; 60/161,148, filed October 22, 1999; and 60/244,119, filed October 26, 2000 all of which are hereby incorporated by reference. In addition, the adapter can be added to an extension probe. The adapter sequence can then be used to target to its complementary capture probe on the surface.

Alternatively, the adapter sequences can be added to other target analytes, to generate unique and reproducible arrays of target analytes in a similar manner. By adding the nucleic acid to the target analyte (for example to an antibody in an immunoassay), the target analytes may then be arrayed.

Accordingly, the present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples; purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the art, virtually any experimental manipulation may have been done on the sample.

The present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. By "target analyte" or "analyte" or grammatical equivalents herein is meant any molecule, compound or particle to be detected. As outlined below, target analytes preferably bind to binding ligands, as is more fully described below. As will be appreciated by those in the art, a large number of analytes may be detected using the present methods; basically, any target analyte for which a binding ligand, described below, may be made may be detected using the methods of the invention.

Suitable analytes include organic and inorganic molecules, including biomolecules. In a preferred embodiment, the analyte may be an environmental pollutant (including pesticides, insecticides, toxins, etc.); a chemical (including solvents, polymers, organic materials, etc.); therapeutic molecules (including therapeutic and abused drugs, antibiotics, etc.); biomolecules (including hormones, cytokines, proteins, lipids, carbohydrates, cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, etc); whole cells (including procaryotic (such as pathogenic bacteria) and eukaryotic cells, including mammalian tumor cells); viruses (including retroviruses, herpesviruses, adenoviruses, lentiviruses, etc.); and spores; etc. Particularly preferred analytes are environmental pollutants; nucleic acids; proteins (including enzymes, antibodies, antigens, growth factors, cytokines, etc); therapeutic and abused drugs; cells; and viruses.

In a preferred embodiment, the target analyte is a protein. As will be appreciated by those in the art,

there are a large number of possible proteinaceous target analytes that may be detected using the present invention. By "proteins" or grammatical equivalents herein is meant proteins, oligopeptides and peptides, derivatives and analogs, including proteins containing non-naturally occurring amino acids and amino acid analogs, and peptidomimetic structures. The side chains may be in either the (R) or the (S) configuration. In a preferred embodiment, the amino acids are in the (S) or L-configuration. As discussed below, when the protein is used as a binding ligand, it may be desirable to utilize protein analogs to retard degradation by sample contaminants.

Suitable protein target analytes include, but are not limited to, (1) immunoglobulins, particularly IgEs, IgGs and IgMs, and particularly therapeutically or diagnostically relevant antibodies, including but not limited to, for example, antibodies to human albumin, apolipoproteins (including apolipoprotein E), human chorionic gonadotropin, cortisol, α-fetoprotein, thyroxin, thyroid stimulating hormone (TSH), antithrombin, antibodies to pharmaceuticals (including antieptileptic drugs (phenytoin, primidone, carbariezepin, ethosuximide, valproic acid, and phenobarbitol), cardioactive drugs (digoxin, lidocaine, procainamide, and disopyramide), bronchodilators (theophylline), antibiotics (chloramphenicol, sulfonamides), antidepressants, immunosuppresants, abused drugs (amphetamine, methamphetamine, cannabinoids, cocaine and opiates) and antibodies to any number of viruses (including orthomyxoviruses, (e.g. influenza virus), paramyxoviruses (e.g respiratory syncytial virus, mumps virus, measles virus), adenoviruses, rhinoviruses, coronaviruses, reoviruses, togaviruses (e.g. rubella virus), parvoviruses, poxviruses (e.g. variola virus, vaccinia virus), enteroviruses (e.g. poliovirus, coxsackievirus), hepatitis viruses (including A, B and C), herpesviruses (e.g. Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus), rotaviruses, Norwalk viruses, hantavirus, arenavirus, rhabdovirus (e.g. rabies virus), retroviruses (including HIV, HTLV-I and -II), papovaviruses (e.g. papillomavirus), polyomaviruses, and picornaviruses, and the like), and bacteria (including a wide variety of pathogenic and non-pathogenic prokaryotes of interest including Bacillus; Vibrio, e.g. *V. cholerae;* Escherichia, e.g. Enterotoxigenic *E. coli*, Shigella, e.g. *S. dysenteriae;* Salmonella, e.g. *S. typhi;* Mycobacterium e.g. *M. tuberculosis, M. leprae*; Clostridium, e.g. *C. botulinum, C. tetani, C. difficile, C.perfringens*; Cornyebacterium, e.g. *C. diphtheriae*; Streptococcus, *S. pyogenes, S. pneumoniae;* Staphylococcus, *e.g. S. aureus*; Haemophilus, e.g. *H. influenzae*; Neisseria, e.g. *N. meningitidis*, *N. gonorrhoeae*; Yersinia, e.g. *G. lambliaY. pestis*, Pseudomonas, e.g. *P. aeruginosa, P. putida*; Chlamydia, e.g. *C. trachomatis*; Bordetella, e.g. *B. pertussis;* Treponema, e.g. *T. palladium;* and the like); (2) enzymes (and other proteins), including but not limited to, enzymes used as indicators of or treatment for heart disease, including creatine kinase, lactate dehydrogenase, aspartate amino transferase, troponin T, myoglobin, fibrinogen, cholesterol, triglycerides, thrombin, tissue plasminogen activator (tPA); pancreatic disease indicators including amylase, lipase, chymotrypsin and trypsin; liver function enzymes and proteins including cholinesterase, bilirubin, and alkaline phosphotase; aldolase, prostatic acid phosphatase, terminal deoxynucleotidyl transferase, and bacterial and viral enzymes such as HIV protease; (3) hormones and cytokines (many of which serve as ligands for cellular receptors) such as erythropoietin (EPO), thrombopoietin (TPO), the interleukins

(including IL-1 through IL-17), insulin, insulin-like growth factors (including IGF-1 and -2), epidermal growth factor (EGF), transforming growth factors (including TGF-α and TGF-β), human growth hormone, transferrin, epidermal growth factor (EGF), low density lipoprotein, high density lipoprotein, leptin, VEGF, PDGF, ciliary neurotrophic factor, prolactin, adrenocorticotropic hormone (ACTH), calcitonin, human chorionic gonadotropin, cotrisol, estradiol, follicle stimulating hormone (FSH), thyroid-stimulating hormone (TSH), leutinzing hormone (LH), progeterone, testosterone, ; and (4) other proteins (including α-fetoprotein, carcinoembryonic antigen CEA.

In addition, any of the biomolecules for which antibodies may be detected may be detected directly as well; that is, detection of virus or bacterial cells, therapeutic and abused drugs, etc., may be done directly.

Suitable target analytes include carbohydrates, including but not limited to, markers for breast cancer (CA15-3, CA 549, CA 27.29), mucin-like carcinoma associated antigen (MCA), ovarian cancer (CA125), pancreatic cancer (DE-PAN-2), and colorectal and pancreatic cancer (CA 19, CA 50, CA242).

In a preferred embodiment, the target analyte (and various adapters and other probes of the invention), comprise nucleic acids. By "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramide (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S.

Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within the definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done to facilitate the addition of labels, alter the hybridization properties of the nucleic acids, or to increase the stability and half-life of such molecules in physiological environments.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made. Alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occuring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (Tm) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in Tm for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. This allows for better detection of mismatches. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xathanine hypoxathanine, isocytosine, isoguanine, etc. A preferred embodiment utilizes isocytosine and isoguanine in nucleic acids designed to be complementary to other probes, rather than target sequences, as this reduces non-specific hybridization, as is generally described in U.S. Patent No. 5,681,702. As used herein, the term "nucleoside" includes nucleotides as well as nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occuring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

In general, probes of the present invention (including adapter sequences and capture probes, described below) are designed to be complementary to a target sequence (either the target sequence of the sample or to other probe sequences, for example adapter sequences) such that hybridization of the target and the probes of the present invention occurs. This complementarity need not be perfect;

there may be any number of base pair mismatches that will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under the selected reaction conditions.

When nucleic acids are to be detected, they are referred to herein as "target nucleic acids" or "target sequences". The term "target sequence" or "target nucleic acid" or grammatical equivalents herein means a nucleic acid sequence on a single strand of nucleic acid. The target sequence may be a portion of a gene, a regulatory sequence, genomic DNA, cDNA, RNA including mRNA and rRNA, or others. As is outlined herein, the target sequence may be a target sequence from a sample, or a derivative target such as a product of a reaction such as a detection sequence from an Invader™ reaction, a ligated probe from an OLA reaction, an extended probe from an SBE reaction, etc. It may be any length, with the understanding that longer sequences are more specific. As will be appreciated by those in the art, the complementary target sequence may take many forms. For example, it may be contained within a larger nucleic acid sequence, i.e. all or part of a gene or mRNA, a restriction fragment of a plasmid or genomic DNA, among others. As is outlined more fully below, probes are made to hybridize to target sequences to determine the presence or absence of the target sequence in a sample. Generally speaking, this term will be understood by those skilled in the art. The target sequence may also be comprised of different target domains; for example, a first target domain of the sample target sequence may hybridize to a capture probe, a second target domain may hybridize to a portion of a label probe, etc. The target domains may be adjacent or separated as indicated. Unless specified, the terms "first" and "second" are not meant to confer an orientation of the sequences with respect to the 5'-3' orientation of the target sequence. For example, assuming a 5'-3' orientation of the complementary target sequence, the first target domain may be located either 5' to the second domain, or 3' to the second domain. In addition, as will be appreciated by those in the art, the probes on the surface of the array (e.g. attached to the microspheres) may be attached in either orientation, either such that they have a free 3' end or a free 5' end.

As is more fully outlined below, the target sequence may comprise a position for which sequence information is desired, generally referred to herein as the "detection position" or "detection locus". In a preferred embodiment, the detection position is a single nucleotide, although in some embodiments, it may comprise a plurality of nucleotides, either contiguous with each other or separated by one or more nucleotides. By "plurality" as used herein is meant at least two. As used herein, the base which basepairs with a detection position base in a hybrid is termed a "readout position" or an "interrogation position".

In some embodiments, as is outlined herein, the target sequence may not be the sample target

sequence but instead is a product of a reaction herein, sometimes referred to herein as a "secondary" or "derivative" target sequence. Thus, for example, in SBE, the extended primer may serve as the target sequence; similarly, in invasive cleavage variations, the cleaved detection sequence may serve as the target sequence.

If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification as needed, as will be appreciated by those in the art.

Once prepared, the target sequence can be used in a variety of reactions for a variety of reasons. For example, in a preferred embodiment, genotyping reactions are done. Similarly, these reactions can also be used to detect the presence or absence of a target sequence. Sequencing or amplification reactions are also preferred. In addition, in any reaction, quantitation of the amount of a target sequence may be done.

Furthermore, as outlined below for each reaction, many of these techniques may be used in a solution based assay, wherein the reaction is done in solution and a reaction product is bound to the array for subsequent detection, or in solid phase assays, where the reaction occurs on the surface and is detected.

In general, the present invention provides pairs of capture probes (nucleic acids that are attached to addresses on arrays) and adapter sequences (sequences that are either perfectly or substantially complementary to the capture probe sequences) that can be used in a wide variety of ways, to immobilize target nucleic acids (either primary targets, such as genomic DNA, mRNA or cDNA, or secondary targets such as amplicons from a nucleic acid amplification or extension reaction, as outlined herein) to the addresses of the array. Thus, all the sequences in the Tables include their complements, and either sequence can be used as a capture probe (e.g. spotted onto a surface or attached to a microsphere of an array) or as the adapter sequence that binds to the capture probe.

Accordingly, by "adapter sequences" or "adapters" or grammatical equivalents is meant a nucleic acid segment generally non-native or exogenous to a target molecule that is used to immobilize the target molecule to a solid support via binding to a capture probe sequence. In a preferred embodiment the adapter sequences and capture probes are selected from the sequences set forth in Table I, Table II, Table III or Table IV.

Table I includes the sequence of the preferred 4000 sequences labeled "Decoder (5'-3')", and inherent in this table are the complementary sequences as well. In addition, the invention includes oligonucleotides that are complementary to those depicted in Table 1.

Table II includes the sequence of the preferred adapter/capture probe sequences and their complementary sequence. Table 2 depicts a preferred subset of 3172 decoder oligonucleotides and their complementary probe oligonucleotides. Accordingly, the invention provides compositions comprising a sequence as outlined in Table 2. In addition, the invention provides a composition comprising a complementary binding pair as outlined in Table 2.

Table 3 includes a preferred subset of 768 decoder oligonucleotides and complementary probe sequences. In some embodiments it may be desirable to include a uniform base at a terminus of the oligonucleotide, such as a T at the 5' end as depicted in Table 4. The inclusion of this uniform or constant base facilitates uniform labeling of the oligonucleotides.

These sequences are used as decoder probes, capture probes or adapter sequences as outlined in U.S.S.N. 09/344,526 and PCT/US99/14387, and U.S.S.N.s 60/160,917 and 09/5656,463 all of which are expressly incorporated by reference in their entirety.

As will be appreciated by those in the art, the length of the capture probe/adapter sequences will vary, depending on the desired "strength" of binding and the number of different adapters desired. In a preferred embodiment, adapter sequences range from about 5 to about 500 basepairs in length, with from about 8 to about 100 being preferred, and from about 10 to about 50 being particularly preferred.

As will be appreciated by those in the art, it is desirable to have adapter sequences that do not have significant homology to naturally occurring target sequences, to avoid non-specific or erroneous binding of target sequences to the capture probes. Accordingly, preferred embodiments utilize some method to select useful adapter sequences. In a preferred embodiment the method is outlined in Figure 1. Briefly, random 24-mer (or could be any desired length as outlined herein), sequences were assembled and subjected to certain defined screening procedures including such steps as requiring that the Tm of each of the sequence be within a pre-defined range. In addition the GC content must be balanced with the AT content and the self-complementarity must be minimized. In addition GC runs should be minimized, that is, runs of Gs or Cs should be reduced. In addition, decoder (adapter) to decoder (adapter) complementarity should be reduced so that the adapters do not hybridize with each other. Finally, the sequences are screened against a specified genomic database. In a preferred embodiment the adapters comprise at least one sequence selected from the sequences in Table I, Table II, Table III or Table IV.

In a preferred embodiment, the adapter sequences are chosen on the basis of a decoding step. As is more fully outlined below, a decoding step is used to decode random bead arrays. In this embodiment, a set of candidate capture probes is chosen; this may be done in a variety of ways. In a preferred embodiment, the sequences are generated randomly, each of a sufficient length to ensure a

low probability of occurring naturally. In some embodiments, for example when the array will be used with a particular organism's genome (e.g. the human genome, the Drosophila genome, etc.), the sequences are compared to the genome as a first filter, for example to remove sequences that would cross hybridize. Additionally, further filtering may be done using well-known methods, such as known methods for selecting good PCR primers. These techniques generally include steps that remove sequences that may have a propensity to form secondary structures or otherwise to cross-hybridize. Additionally, sequences that have extremes of melting temperatures can be optionally discarded, depending on the planned assay conditions.

Once a set of candidate capture probes is obtained, an array comprising the capture probes is made, and a matching set of decoding probes comprising the adapter sequences (e.g. the complements of the capture probes), as more fully outlined below, is made. Decoding then proceeds. Probes that do not hybridize well, for whatever reason, will not decode well, generally due to weak signals, and are generally discarded. Probes that cross-hybridize will also not decode well, as they will give ambiguous or mixed decoding signals. Only probes that hybridize sufficiently strongly and specifically will decode. Thus, by setting suitable thresholds for signal strength and signal purity, adapter sequences that perform according to specified criteria are identified. Additionally, by setting a range on signal strength, capture probe/adapter sequence pairs that perform similarly (but hybridize specifically) are identified. In a preferred embodiment, decoding reactions are repeated, under a variety of conditions, to test the robustness of the sequence pair.

Once identified, the adapter sequences are added to target sequences in a variety of ways, as will be appreciated by those in the art. In a preferred embodiment, nucleic acid amplification reactions are done, as is generally outlined in "Detection of Nucleic Acid Amplification Reactions Using Bead Arrays" and "Sequence Determination of Nucleic Acids using Arrays with Microspheres", both of which were filed on October 22, 1999, (U.S.S.N.'s 60/161,148 and 09/425,633, respectively), both of which are hereby incorporated by reference in their entirety. These may be either target amplification or signal amplification. In general, the techniques can be described as follows. Most amplification techniques require one or more primers hybridizing to all or part the target sequence (e.g. that hybridize to a target domain). The adapter sequences can be added to one or more of the primers (depending on the configuration/orientation of the system and need) and the amplification reactions are run. Thus, for example, PCR primers comprising at least one adapter sequence (and preferably one on each PCR primer) may be used; one or both of the ligation probes of an OLA or LCR reaction may comprise an adapter sequence; the sequencing primers for pyrosequencing, single-base extension, reversible chain termination, etc., reactions may comprise an adapter sequence; either the invader probe or the signalling probe of invasive cleavage reactions can comprise an adapter sequence; etc. Similarly, for signal detection techniques, the probes may comprise adapter sequences, with preferred methods utilizing removal of the unreacted probes. In addition, primers may include universal priming sequences. That is, the adapters may additionally contain universal priming sequences for universal

amplification of products of any of the reactions described herein. Universal priming sequences are further outlined in 09/779376, filed February 7, 2001; 09/779202, filed February 7, 2001; 09/915231, filed July 24, 2001; 60/180810, filed February 7, 2000; and 60/297609, filed June 11, 2001; and 60/311194 filed August 9, 2001, all of which are expressly incorporated herein by reference.

In an alternative embodiment, non-nucleic acid reactions are used to add adapter sequences to the nucleic acid targets. For example, for the direct detection of non-amplified target sequences (e.g. genomic DNA samples, etc.) on universal arrays, non-amplification methods are required. In this embodiment, binding partner pairs or chemical methods may be used. For example, one member of a binding partner pair may be attached to the adapter sequence and the other member attached to the target sequence. For example, the binding partner be a hapten or antigen, which will bind its binding partner. For example, suitable binding partner pairs include, but are not limited to: antigens (such as proteins (including peptides)) and antibodies (including fragments thereof (FAbs, etc.)); proteins and small molecules, including biotin/streptavidin and digoxygenin and antibodies; enzymes and substrates or inhibitors; other protein-protein interacting pairs; receptor-ligands; and carbohydrates and their binding partners, are also suitable binding pairs. Nucleic acid - nucleic acid binding proteins pairs are also useful. In general, the smaller of the pair is attached to the NTP (or the probe) for incorporation into the extension primer. Preferred binding partner pairs include, but are not limited to, biotin (or imino-biotin) and streptavidin, digeoxinin and Abs, and Prolinx™ reagents.

In a preferred embodiment, chemical attachment methods are used. In this embodiment, chemical functional groups on each of the target sequences and adapter sequences are used. As is known in the art, this may be accomplished in a variety of ways. Preferred functional groups for attachment are amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the two sequences are joined together; for example, amino groups on each nucleic acid may be attached, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference).

In a preferred embodiment, aptamers are used in the system. Aptamers are nucleic acids that can be made to bind to virtually any target analyte; see Bock et al., Nature 355:564 (1992); Femulok et al., Current Op. Chem. Biol. 2:230 (1998); and U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867,5,705,337, and related patents, hereby incorporated by reference.

In a preferred embodiment, an array comprising capture probes that hybridize to adapter sequences is made, as outlined herein. In one embodiment aptamers, comprising adapter sequences, can be added. As will be appreciated by those in the art, the aptamers may be preassociated with their binding partners, e.g. target analytes, prior to introduction to the array, or not. In addition, the association between the adapter sequences on the aptamers and the capture probes can be made

covalent, for example through the use of reactive groups (e.g. psoralen) and appropriate activation.

In addition, the present invention is directed to the use of adapter sequences to assemble arrays comprising other target analytes.

The adapter sequences may be chosen as outlined above. Preferably the adapters are selected from the sequences set forth in Table I, Table II, Table III or Table IV. These adapter sequences can then be added to the target analytes using a variety of techniques. In general, as described above, non-covalent attachment using binding partner pairs may be done, or covalent attachment using chemical moieties (including linkers).

Advantages of using adapters include but are not limited to, for example, the ability to create universal arrays. That is, a single array is utilized with each capture probe designed to hybridize with a specific adapter. The adapters are joined to any number of target analytes, such as nucleic acids, as is described herein. Thus, the same array is used for vastly different target analytes. Furthermore, hybridization of adapters with capture probes results in non-covalent attachment of the target nucleic acid to the address of the array (e.g. a microsphere in some embodiments). As such, the target nucleic/adapter hybrid is easily removed, and the microsphere/capture probe can be re-used. In addition, the construction of kits is greatly facilitated by the use of adapters. For example, arrays or microspheres can be prepared that comprise the capture probe; the adapters can be packaged along with the microspheres for attachment to any target analyte of interest. Thus, one need only attach the adapter to the target analyte and disperse on the array for the construction of an array of target analytes.

Accordingly the present invention provides kits comprising adapters. Preferably the kits include at least 1 nucleic acid sequence as set forth in Table 1. More preferably the kits include at least 10-25 nucleic acids, with at least 50 nucleic acids more preferred. Even more preferable are kits that include at least 100 nucleic acids with more than 1000 even more preferred and more than 2000 even more preferred.

It should also be noted that the sequences defined herein can also be used in "sandwich" assay formats, wherein a capture extender probe comprising a first domain that will hybridize to the capture probe and a second domain that has a target specific domain is used. The capture extender probe hybridizes both to the target sequence and the capture probe, thereby immobilizing the target sequence on the array.

Once the adapter sequences are associated with the target analyte, including target nucleic acids, the compositions are added to an array comprising addresses comprising capture probes. In one embodiment a plurality of hybrid adapter sequence/target analytes are pooled prior to addition to an

array. All of the methods and compositions herein are drawn to compositions and methods for detecting the presence of target analytes, particularly nucleic acids, using adapter arrays.

Accordingly, the present invention provides array compositions comprising at least a first substrate with a surface comprising individual sites. The present system finds particular utility in array formats, i.e. wherein there is a matrix of capture probes (herein generally referred to "pads", "addresses" or "micro-locations"). By "array" or "biochip" herein is meant a plurality of nucleic acids in an array format; the size of the array will depend on the composition and end use of the array. Nucleic acids arrays are known in the art, and can be classified in a number of ways; both ordered arrays (e.g. the ability to resolve chemistries at discrete sites), and random arrays are included. Ordered arrays include, but are not limited to, those made using photolithography techniques (Affymetrix GeneChip™), spotting techniques (Synteni and others), printing techniques (Hewlett Packard and Rosetta), three dimensional "gel pad" arrays, etc. In one embodiment the ordered arrays include arrays that contain nucleic acids at known locations. That is, the adapters or capture probes described herein are immobilized at known locations on a substrate. By "known" locations is meant a site that is known or has been known.

In addition, adapters find use "liquid arrays". By "liquid arrays" is meant an array in solution for analysis, for example, by flow cytometry.

A preferred embodiment utilizes microspheres on a variety of substrates including fiber optic bundles, as are outlined in PCTs US98/21193, PCT US99/14387 and PCT US98/05025; WO98/50782; and U.S.S.N.s 09/287,573, 09/151,877, 09/256,943, 09/316,154, 60/119,323, 09/315,584; all of which are expressly incorporated by reference. While much of the discussion below is directed to the use of microsphere arrays on fiber optic bundles, any array format of nucleic acids on solid supports may be utilized.

Arrays containing from about 2 different bioactive agents (e.g. different beads, when beads are used) to many millions can be made, with very large arrays being possible. Generally, the array will comprise from two to as many as a billion or more, depending on the size of the beads and the substrate, as well as the end use of the array, thus very high density, high density, moderate density, low density and very low density arrays may be made. Preferred ranges for very high density arrays are from about 10,000,000 to about 2,000,000,000, with from about 100,000,000 to about 1,000,000,000 being preferred (all numbers being in square cm). High density arrays range about 100,000 to about 10,000,000, with from about 1,000,000 to about 5,000,000 being particularly preferred. Moderate density arrays range from about 10,000 to about 100,000 being particularly preferred, and from about 20,000 to about 50,000 being especially preferred. Low density arrays are generally less than 10,000, with from about 1,000 to about 5,000 being preferred. Very low density arrays are less than 1,000, with from about 10 to about 1000 being preferred, and from about 100 to about 500 being particularly preferred. In some embodiments, the compositions of the invention may

not be in array format; that is, for some embodiments, compositions comprising a single bioactive agent may be made as well. In addition, in some arrays, multiple substrates may be used, either of different or identical compositions. Thus for example, large arrays may comprise a plurality of smaller substrates.

In addition, one advantage of the present compositions is that particularly through the use of fiber optic technology, extremely high density arrays can be made. Thus for example, because beads of 200 μm or less (with beads of 200 nm possible) can be used, and very small fibers are known, it is possible to have as many as 40,000 or more (in some instances, 1 million) different elements (e.g. fibers and beads) in a 1 mm^2 fiber optic bundle, with densities of greater than 25,000,000 individual beads and fibers (again, in some instances as many as 50-100 million) per 0.5 cm^2 obtainable (4 million per square cm for 5 μ center-to-center and 100 million per square cm for 1 μ center-to-center).

By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of beads and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates is very large. Possible substrates include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers. In general, the substrates allow optical detection and do not themselves appreciably fluoresce.

Generally the substrate is flat (planar), although as will be appreciated by those in the art, other configurations of substrates may be used as well; for example, three dimensional configurations can be used, for example by embedding the beads in a porous block of plastic that allows sample access to the beads and using a confocal microscope for detection. Similarly, the beads may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Preferred substrates include optical fiber bundles as discussed below, and flat planar substrates such as glass, polystyrene and other plastics and acrylics.

In a preferred embodiment, the substrate is an optical fiber bundle or array, as is generally described in U.S.S.N.s 08/944,850 and 08/519,062, PCT US98/05025, and PCT US98/09163, all of which are expressly incorporated herein by reference. Preferred embodiments utilize preformed unitary fiber optic arrays. By "preformed unitary fiber optic array" herein is meant an array of discrete individual fiber optic strands that are co-axially disposed and joined along their lengths. The fiber strands are generally individually clad. However, one thing that distinguished a preformed unitary array from other fiber optic formats is that the fibers are not individually physically manipulatable; that is, one strand

generally cannot be physically separated at any point along its length from another fiber strand.

At least one surface of the substrate is modified to contain discrete, individual sites for later association of microspheres. These sites may comprise physically altered sites, i.e. physical configurations such as wells or small depressions in the substrate that can retain the beads, such that a microsphere can rest in the well, or the use of other forces (magnetic or compressive), or chemically altered or active sites, such as chemically functionalized sites, electrostatically altered sites, hydrophobically/ hydrophilically functionalized sites, spots of adhesive, etc.

The sites may be a pattern, i.e. a regular design or configuration, or randomly distributed. A preferred embodiment utilizes a regular pattern of sites such that the sites may be addressed in the X-Y coordinate plane. "Pattern" in this sense includes a repeating unit cell, preferably one that allows a high density of beads on the substrate. However, it should be noted that these sites may not be discrete sites. That is, it is possible to use a uniform surface of adhesive or chemical functionalities, for example, that allows the attachment of beads at any position. That is, the surface of the substrate is modified to allow attachment of the microspheres at individual sites, whether or not those sites are contiguous or non-contiguous with other sites. Thus, the surface of the substrate may be modified such that discrete sites are formed that can only have a single associated bead, or alternatively, the surface of the substrate is modified and beads may go down anywhere, but they end up at discrete sites.

In a preferred embodiment, the surface of the substrate is modified to contain wells, i.e. depressions in the surface of the substrate. This may be done as is generally known in the art using a variety of techniques, including, but not limited to, photolithography, stamping techniques, molding techniques and microetching techniques. As will be appreciated by those in the art, the technique used will depend on the composition and shape of the substrate.

In a preferred embodiment, physical alterations are made in a surface of the substrate to produce the sites. In a preferred embodiment, the substrate is a fiber optic bundle and the surface of the substrate is a terminal end of the fiber bundle, as is generally described in 08/818,199 and 09/151,877, both of which are hereby expressly incorporated by reference. In this embodiment, wells are made in a terminal or distal end of a fiber optic bundle comprising individual fibers. In this embodiment, the cores of the individual fibers are etched, with respect to the cladding, such that small wells or depressions are formed at one end of the fibers. The required depth of the wells will depend on the size of the beads to be added to the wells.

Generally in this embodiment, the microspheres are non-covalently associated in the wells, although the wells may additionally be chemically functionalized as is generally described below, cross-linking agents may be used, or a physical barrier may be used, i.e. a film or membrane over the beads.

In a preferred embodiment, the surface of the substrate is modified to contain chemically modified sites, that can be used to attach, either covalently or non-covalently, the microspheres of the invention to the discrete sites or locations on the substrate. "Chemically modified sites" in this context includes, but is not limited to, the addition of a pattern of chemical functional groups including amino groups, carboxy groups, oxo groups and thiol groups, that can be used to covalently attach microspheres, which generally also contain corresponding reactive functional groups; the addition of a pattern of adhesive that can be used to bind the microspheres (either by prior chemical functionalization for the addition of the adhesive or direct addition of the adhesive); the addition of a pattern of charged groups (similar to the chemical functionalities) for the electrostatic attachment of the microspheres, i.e. when the microspheres comprise charged groups opposite to the sites; the addition of a pattern of chemical functional groups that renders the sites differentially hydrophobic or hydrophilic, such that the addition of similarly hydrophobic or hydrophilic microspheres under suitable experimental conditions will result in association of the microspheres to the sites on the basis of hydroaffinity. For example, the use of hydrophobic sites with hydrophobic beads, in an aqueous system, drives the association of the beads preferentially onto the sites. As outlined above, "pattern" in this sense includes the use of a uniform treatment of the surface to allow attachment of the beads at discrete sites, as well as treatment of the surface resulting in discrete sites. As will be appreciated by those in the art, this may be accomplished in a variety of ways.

In a preferred embodiment, the compositions of the invention further comprise a population of microspheres. By "population" herein is meant a plurality of beads as outlined above for arrays. Within the population are separate subpopulations, which can be a single microsphere or multiple identical microspheres. That is, in some embodiments, as is more fully outlined below, the array may contain only a single bead for each capture probe; preferred embodiments utilize a plurality of beads of each type.

By "microspheres" or "beads" or "particles" or grammatical equivalents herein is meant small discrete particles. The composition of the beads will vary, depending on the class of capture probe and the method of synthesis. Suitable bead compositions include those used in peptide, nucleic acid and organic moiety synthesis, including, but not limited to, plastics, ceramics, glass, polystyrene, methylstyrene, acrylic polymers, paramagnetic materials, thoria sol, carbon graphite, titanium dioxide, latex or cross-linked dextrans such as Sepharose, cellulose, nylon, cross-linked micelles and Teflon may all be used. *"Microsphere Detection Guide"* from Bangs Laboratories, Fishers IN is a helpful guide.

The beads need not be spherical; irregular particles may be used. In addition, the beads may be porous, thus increasing the surface area of the bead available for either capture probe attachment or tag attachment. The bead sizes range from nanometers, i.e. 100 nm, to millimeters, i.e. 1 mm, with beads from about 0.2 micron to about 200 microns being preferred, and from about 0.5 to about 5

micron being particularly preferred, although in some embodiments smaller beads may be used.

It should be noted that a key component of this embodiment of the invention is the use of a substrate/bead pairing that allows the association or attachment of the beads at discrete sites on the surface of the substrate, such that the beads do not move during the course of the assay.

Each microsphere comprises a capture probe, although as will be appreciated by those in the art, there may be some microspheres which do not contain a capture probe, depending on the synthetic methods. Alternatively, some have more than one capture probe.

Attachment of the nucleic acids may be done in a variety of ways, as will be appreciated by those in the art, including, but not limited to, chemical or affinity capture (for example, including the incorporation of derivatized nucleotides such as AminoLink or biotinylated nucleotides that can then be used to attach the nucleic acid to a surface, as well as affinity capture by hybridization), cross-linking, and electrostatic attachment, etc. In a preferred embodiment, affinity capture is used to attach the nucleic acids to the beads. For example, nucleic acids can be derivatized, for example with one member of a binding pair, and the beads derivatized with the other member of a binding pair. Suitable binding pairs are as described herein for IBL/DBL pairs. For example, the nucleic acids may be biotinylated (for example using enzymatic incorporate of biotinylated nucleotides, for by photoactivated cross-linking of biotin). Biotinylated nucleic acids can then be captured on streptavidin-coated beads, as is known in the art. Similarly, other hapten-receptor combinations can be used, such as digoxigenin and anti-digoxigenin antibodies. Alternatively, chemical groups can be added in the form of derivatized nucleotides, that can them be used to add the nucleic acid to the surface.

Preferred attachments are covalent, although even relatively weak interactions (i.e. non-covalent) can be sufficient to attach a nucleic acid to a surface, if there are multiple sites of attachment per each nucleic acid. Thus, for example, electrostatic interactions can be used for attachment, for example by having beads carrying the opposite charge to the bioactive agent.

Similarly, affinity capture utilizing hybridization can be used to attach nucleic acids to beads. For example, as is known in the art, polyA+RNA is routinely captured by hybridization to oligo-dT beads; this may include oligo-dT capture followed by a cross-linking step, such as psoralen crosslinking). If the nucleic acids of interest do not contain a polyA tract, one can be attached by polymerization with terminal transferase, or via ligation of an oligoA linker, as is known in the art.

Alternatively, chemical crosslinking may be done, for example by photoactivated crosslinking of thymidine to reactive groups, as is known in the art.

In a preferred embodiment, each bead comprises a single type of capture probe, although a plurality of

individual capture probes are preferably attached to each bead. Similarly, preferred embodiments utilize more than one microsphere containing a unique capture probe; that is, there is redundancy built into the system by the use of subpopulations of microspheres, each microsphere in the subpopulation containing the same capture probe.

In an alternative embodiment, each bead comprises a plurality of different capture probes.

As will be appreciated by those in the art, the capture probes may either be synthesized directly on the beads, or they may be made and then attached after synthesis. In a preferred embodiment, linkers are used to attach the capture probes to the beads, to allow both good attachment, sufficient flexibility to allow good interaction with the target molecule, and to avoid undesirable binding reactions.

In a preferred embodiment, the capture probes are synthesized directly on the beads. As is known in the art, many classes of chemical compounds are currently synthesized on solid supports, such as peptides, organic moieties, and nucleic acids. It is a relatively straightforward matter to adjust the current synthetic techniques to use beads.

In a preferred embodiment, the capture probes are synthesized first, and then covalently attached to the beads. As will be appreciated by those in the art, this will be done depending on the composition of the capture probes and the beads. The functionalization of solid support surfaces such as certain polymers with chemically reactive groups such as thiols, amines, carboxyls, etc. is generally known in the art. Accordingly, "blank" microspheres may be used that have surface chemistries that facilitate the attachment of the desired functionality by the user. Some examples of these surface chemistries for blank microspheres include, but are not limited to, amino groups including aliphatic and aromatic amines, carboxylic acids, aldehydes, amides, chloromethyl groups, hydrazide, hydroxyl groups, sulfonates and sulfates.

In a preferred embodiment the attachment of nucleic acids to substrates includes contacting the oligonucleotide and the solid support in the presence of high salt concentrations. As is appreciated by those skilled in the art, salt includes, but is not limited to sodium chloride, potassium chloride, calcium chloride, magnesium chloride, lithium chloride, rubidium chloride, cesium chloride, barium chloride and the like. In a preferred embodiment, salt as used in the invention includes sodium chloride.

By high salt concentrations is meant salt that is more concentrated than about 0.1 M salt. In a preferred embodiment, by high salt concentrations is meant greater than about 0.2 M salt. In a particularly preferred embodiment, high salt concentrations include from about 0.5 to 3M salt, with about 1M to 2M being most preferred.

By solid support or other grammatical equivalents herein is meant any material that can be modified

to contain oligonucleotides. As will be appreciated by those in the art, the number of possible solid supports is very large. Possible solid supports include, but are not limited to beads, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers.

Once formed, the support containing the oligonucleotides finds use in a variety of systems including decoding arrays as described in more detail in U.S.S.N. 09/344,526, and U.S.S.N. 09/574, 117, both of which are expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in microfluidic systems as described in U.S.S.N. 09/306,369 which is expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in composite array systems as described in U.S.S.N. 09/606,369, which is expressly incorporated herein by reference. In addition the support containing the oligonucleotides finds use in a variety of assays as outlined in more detail in U.S.S.N.s 09/513,362, 09/517,945, 09/535,854, 60/160,917, 60/180,810, 60/182,955, and 09/566,463, all of which are expressly incorporated herein by reference in their entirety. In addition, the support containing the oligonucleotides finds use in array based sensors as described in more detail in 09/287,573, 09/260,963, 09/450,829, 09/151,877, 09/187,289 and 08/519,062, all of which are expressly incorporated herein by reference in their entirety.

Accordingly the invention provides a method of attaching oligonucleotides to a solid support. The method includes contacting the oligonucleotides with the support in the presence of high salt as described herein. Once attached, as discussed in the examples, the attached oligonucleotides readily hybridize to targets, probes and the like. Attachment of crude oligonucleotides in the presence of high salt is as efficient as attaching purified oligonucleotides. Thus, the invention also contemplates a method of attachment of oligonucleotides to a solid support without prior purification of the oligonucleotides. Again, the method includes contacting the crude oligonucleotides with a solid support in the presence of high salt as described herein.

The capture probes are designed to be substantially complementary to the adapter sequences, to allow for a minimum of cross reactivity.

When microsphere arrays are used, an encoding/decoding system must be used. That is, since the beads are generally put onto the substrate randomly, there are several ways to correlate the functionality on the bead with its location, including the incorporation of unique optical signatures, generally fluorescent dyes, that could be used to identify the chemical functionality on any particular bead. This allows the synthesis of the candidate agents (i.e. compounds such as nucleic acids and

antibodies) to be divorced from their placement on an array, i.e. the candidate agents may be synthesized on the beads, and then the beads are randomly distributed on a patterned surface. Since the beads are first coded with an optical signature, this means that the array can later be "decoded", i.e. after the array is made, a correlation of the location of an individual site on the array with the bead or candidate agent at that particular site can be made. This means that the beads may be randomly distributed on the array, a fast and inexpensive process as compared to either the in situ synthesis or spotting techniques of the prior art.

However, the drawback to these methods is that for a large array, the system requires a large number of different optical signatures, which may be difficult or time-consuming to utilize. Accordingly, the present invention provides several improvements over these methods, generally directed to methods of coding and decoding the arrays. That is, as will be appreciated by those in the art, the placement of the capture probes is generally random, and thus a coding/decoding system is required to identify the probe at each location in the array. This may be done in a variety of ways, as is more fully outlined below, and generally includes: a) the use a decoding binding ligand (DBL), generally directly labeled, that binds to either the capture probe or to identifier binding ligands (IBLs) attached to the beads; b) positional decoding, for example by either targeting the placement of beads (for example by using photoactivatible or photocleavable moieties to allow the selective addition of beads to particular locations), or by using either sub-bundles or selective loading of the sites, as are more fully outlined below; c) selective decoding, wherein only those beads that bind to a target are decoded; or d) combinations of any of these. In some cases, as is more fully outlined below, this decoding may occur for all the beads, or only for those that bind a particular target sequence. Similarly, this may occur either prior to or after addition of a target sequence. In addition, as outlined herein, the target sequences detected may be either a primary target sequence (e.g. a patient sample), or a reaction product from one of the methods described herein (e.g. an extended SBE probe, a ligated probe, a cleaved signal probe, etc.).

Once the identity (i.e. the actual agent) and location of each microsphere in the array has been fixed, the array is exposed to samples containing the target sequences, although as outlined below, this can be done prior to or during the analysis as well. The target sequences can hybridize (either directly or indirectly) to the capture probes as is more fully outlined below, and results in a change in the optical signal of a particular bead.

In the present invention, "decoding" may not rely on the use of optical signatures, but rather on the use of decoding binding ligands that are added during a decoding step. The decoding binding ligands will bind either to a distinct identifier binding ligand partner that is placed on the beads, or to the capture probe itself. In this embodiment the decoding binding ligand either is complementary to the capture probe. In this embodiment the decoding binding ligand has the sequence of the adapter that also binds to the capture probe. In a preferred embodiment the decoder binding ligand is a nucleic acid

that has the sequence of at least one of the nucleic acids set forth in Table 1.

The decoding binding ligands are either directly or indirectly labeled, and thus decoding occurs by detecting the presence of the label. By using pools of decoding binding ligands in a sequential fashion, it is possible to greatly minimize the number of required decoding steps.

In some embodiments, the microspheres may additionally comprise identifier binding ligands for use in certain decoding systems. By "identifier binding ligands" or "IBLs" herein is meant a compound that will specifically bind a corresponding decoder binding ligand (DBL) to facilitate the elucidation of the identity of the capture probe attached to the bead. That is, the IBL and the corresponding DBL form a binding partner pair. By "specifically bind" herein is meant that the IBL binds its DBL with specificity sufficient to differentiate between the corresponding DBL and other DBLs (that is, DBLs for other IBLs), or other components or contaminants of the system. The binding should be sufficient to remain bound under the conditions of the decoding step, including wash steps to remove non-specific binding. In some embodiments, for example when the IBLs and corresponding DBLs are proteins or nucleic acids, the dissociation constants of the IBL to its DBL will be less than about 10^{-4}-10^{-6} M^{-1}, with less than about 10^{-5} to 10^{-9} M^{-1} being preferred and less than about 10^{-7} -10^{-9} M^{-1} being particularly preferred.

IBL-DBL binding pairs are known or can be readily found using known techniques. For example, when the IBL is a protein, the DBLs include proteins (particularly including antibodies or fragments thereof (FAbs, etc.)) or small molecules, or vice versa (the IBL is an antibody and the DBL is a protein). Metal ion- metal ion ligands or chelators pairs are also useful. Antigen-antibody pairs, enzymes and substrates or inhibitors, other protein-protein interacting pairs, receptor-ligands, complementary nucleic acids, and carbohydrates and their binding partners are also suitable binding pairs. Nucleic acid - nucleic acid binding proteins pairs are also useful. Similarly, as is generally described in U.S. Patents 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867,5,705,337, and related patents, hereby incorporated by reference, nucleic acid "aptamers" can be developed for binding to virtually any target; such an aptamer-target pair can be used as the IBL-DBL pair. Similarly, there is a wide body of literature relating to the development of binding pairs based on combinatorial chemistry methods.

In a preferred embodiment, the IBL is a molecule whose color or luminescence properties change in the presence of a selectively-binding DBL. For example, the IBL may be a fluorescent pH indicator whose emission intensity changes with pH. Similarly, the IBL may be a fluorescent ion indicator, whose emission properties change with ion concentration.

Alternatively, the IBL is a molecule whose color or luminescence properties change in the presence of various solvents. For example, the IBL may be a fluorescent molecule such as an ethidium salt whose

fluorescence intensity increases in hydrophobic environments. Similarly, the IBL may be a derivative of fluorescein whose color changes between aqueous and nonpolar solvents.

In one embodiment, the DBL may be attached to a bead, i.e. a "decoder bead", that may carry a label such as a fluorophore.

In a preferred embodiment, the IBL-DBL pair comprise substantially complementary single-stranded nucleic acids. In this embodiment, the binding ligands can be referred to as "identifier probes" and "decoder probes". Generally, the identifier and decoder probes range from about 4 basepairs in length to about 1000, with from about 6 to about 100 being preferred, and from about 8 to about 40 being particularly preferred. What is important is that the probes are long enough to be specific, i.e. to distinguish between different IBL-DBL pairs, yet short enough to allow both a) dissociation, if necessary, under suitable experimental conditions, and b) efficient hybridization.

In a preferred embodiment, as is more fully outlined below, the IBLs do not bind to DBLs. Rather, the IBLs are used as identifier moieties ("IMs") that are identified directly, for example through the use of mass spectroscopy.

Alternatively, in a preferred embodiment, the IBL and the capture probe are the same moiety; thus, for example, as outlined herein, particularly when no optical signatures are used, the capture probe can serve as both the identifier and the agent. For example, in the case of nucleic acids, the bead-bound probe (which serves as the capture probe) can also bind decoder probes, to identify the sequence of the probe on the bead. Thus, in this embodiment, the DBLs bind to the capture probes.

In one embodiment, the microspheres may contain an optical signature. That is, as outlined in U.S.S.N.s 08/818,199 and 09/151,877, previous work had each subpopulation of microspheres comprising a unique optical signature or optical tag that is used to identify the unique capture probe of that subpopulation of microspheres; that is, decoding utilizes optical properties of the beads such that a bead comprising the unique optical signature may be distinguished from beads at other locations with different optical signatures. Thus the previous work assigned each capture probe a unique optical signature such that any microspheres comprising that capture probe are identifiable on the basis of the signature. These optical signatures comprised dyes, usually chromophores or fluorophores, that were entrapped or attached to the beads themselves. Diversity of optical signatures utilized different fluorochromes, different ratios of mixtures of fluorochromes, and different concentrations (intensities) of fluorochromes.

In a preferred embodiment, the present invention does not rely solely on the use of optical properties to decode the arrays. However, as will be appreciated by those in the art, it is possible in some embodiments to utilize optical signatures as an additional coding method, in conjunction with the

present system. Thus, for example, as is more fully outlined below, the size of the array may be effectively increased while using a single set of decoding moieties in several ways, one of which is the use of optical signatures one some beads. Thus, for example, using one "set" of decoding molecules, the use of two populations of beads, one with an optical signature and one without, allows the effective doubling of the array size. The use of multiple optical signatures similarly increases the possible size of the array.

In a preferred embodiment, each subpopulation of beads comprises a plurality of different IBLs. By using a plurality of different IBLs to encode each capture probe, the number of possible unique codes is substantially increased. That is, by using one unique IBL per capture probe, the size of the array will be the number of unique IBLs (assuming no "reuse" occurs, as outlined below). However, by using a plurality of different IBLs per bead, n, the size of the array can be increased to 2^n, when the presence or absence of each IBL is used as the indicator. For example, the assignment of 10 IBLs per bead generates a 10 bit binary code, where each bit can be designated as "1" (IBL is present) or "0" (IBL is absent). A 10 bit binary code has 2^{10} possible variants However, as is more fully discussed below, the size of the array may be further increased if another parameter is included such as concentration or intensity; thus for example, if two different concentrations of the IBL are used, then the array size increases as 3^n. Thus, in this embodiment, each individual capture probe in the array is assigned a combination of IBLs, which can be added to the beads prior to the addition of the capture probe, after, or during the synthesis of the capture probe, i.e. simultaneous addition of IBLs and capture probe components.

Alternatively, the combination of different IBLs can be used to elucidate the sequence of the nucleic acid. Thus, for example, using two different IBLs (IBL1 and IBL2), the first position of a nucleic acid can be elucidated: for example, adenosine can be represented by the presence of both IBL1 and IBL2; thymidine can be represented by the presence of IBL1 but not IBL2, cytosine can be represented by the presence of IBL2 but not IBL1, and guanosine can be represented by the absence of both. The second position of the nucleic acid can be done in a similar manner using IBL3 and IBL4; thus, the presence of IBL1, IBL2, IBL3 and IBL4 gives a sequence of AA; IBL1, IBL2, and IBL3 shows the sequence AT; IBL1, IBL3 and IBL4 gives the sequence TA, etc. The third position utilizes IBL5 and IBL6, etc. In this way, the use of 20 different identifiers can yield a unique code for every possible 10-mer.

In this way, a sort of "bar code" for each sequence can be constructed; the presence or absence of each distinct IBL will allow the identification of each capture probe.

In addition, the use of different concentrations or densities of IBLs allows a "reuse" of sorts. If, for example, the bead comprising a first agent has a 1X concentration of IBL, and a second bead comprising a second agent has a 10X concentration of IBL, using saturating concentrations of the

corresponding labelled DBL allows the user to distinguish between the two beads.

Once the microspheres comprising the capture probes are generated, they are added to the substrate to form an array. It should be noted that while most of the methods described herein add the beads to the substrate prior to the assay, the order of making, using and decoding the array can vary. For example, the array can be made, decoded, and then the assay done. Alternatively, the array can be made, used in an assay, and then decoded; this may find particular use when only a few beads need be decoded. Alternatively, the beads can be added to the assay mixture, i.e. the sample containing the target sequences, prior to the addition of the beads to the substrate; after addition and assay, the array may be decoded. This is particularly preferred when the sample comprising the beads is agitated or mixed; this can increase the amount of target sequence bound to the beads per unit time, and thus (in the case of nucleic acid assays) increase the hybridization kinetics. This may find particular use in cases where the concentration of target sequence in the sample is low; generally, for low concentrations, long binding times must be used.

In general, the methods of making the arrays and of decoding the arrays is done to maximize the number of different candidate agents that can be uniquely encoded. The compositions of the invention may be made in a variety of ways. In general, the arrays are made by adding a solution or slurry comprising the beads to a surface containing the sites for attachment of the beads. This may be done in a variety of buffers, including aqueous and organic solvents, and mixtures. The solvent can evaporate, and excess beads are removed.

In a preferred embodiment, when non-covalent methods are used to associate the beads with the array, a novel method of loading the beads onto the array is used. This method comprises exposing the array to a solution of particles (including microspheres and cells) and then applying energy, e.g. agitating or vibrating the mixture. This results in an array comprising more tightly associated particles, as the agitation is done with sufficient energy to cause weakly-associated beads to fall off (or out, in the case of wells). These sites are then available to bind a different bead. In this way, beads that exhibit a high affinity for the sites are selected. Arrays made in this way have two main advantages as compared to a more static loading: first of all, a higher percentage of the sites can be filled easily, and secondly, the arrays thus loaded show a substantial decrease in bead loss during assays. Thus, in a preferred embodiment, these methods are used to generate arrays that have at least about 50% of the sites filled, with at least about 75% being preferred, and at least about 90% being particularly preferred. Similarly, arrays generated in this manner preferably lose less than about 20% of the beads during an assay, with less than about 10% being preferred and less than about 5% being particularly preferred.

In this embodiment, the substrate comprising the surface with the discrete sites is immersed into a solution comprising the particles (beads, cells, etc.). The surface may comprise wells, as is described

herein, or other types of sites on a patterned surface such that there is a differential affinity for the sites. This differnetial affinity results in a competitive process, such that particles that will associate more tightly are selected. Preferably, the entire surface to be "loaded" with beads is in fluid contact with the solution. This solution is generally a slurry ranging from about 10,000:1 beads:solution (vol:vol) to 1:1. Generally, the solution can comprise any number of reagents, including aqueous buffers, organic solvents, salts, other reagent components, etc. In addition, the solution preferably comprises an excess of beads; that is, there are more beads than sites on the array. Preferred embodiments utilize two-fold to billion-fold excess of beads.

The immersion can mimic the assay conditions; for example, if the array is to be "dipped" from above into a microtiter plate comprising samples, this configuration can be repeated for the loading, thus minimizing the beads that are likely to fall out due to gravity.

Once the surface has been immersed, the substrate, the solution, or both are subjected to a competitive process, whereby the particles with lower affinity can be disassociated from the substrate and replaced by particles exhibiting a higher affinity to the site. This competitive process is done by the introduction of energy, in the form of heat, sonication, stirring or mixing, vibrating or agitating the solution or substrate, or both.

A preferred embodiment utilizes agitation or vibration. In general, the amount of manipulation of the substrate is minimized to prevent damage to the array; thus, preferred embodiments utilize the agitation of the solution rather than the array, although either will work. As will be appreciated by those in the art, this agitation can take on any number of forms, with a preferred embodiment utilizing microtiter plates comprising bead solutions being agitated using microtiter plate shakers.

The agitation proceeds for a period of time sufficient to load the array to a desired fill. Depending on the size and concentration of the beads and the size of the array, this time may range from about 1 second to days, with from about 1 minute to about 24 hours being preferred.

It should be noted that not all sites of an array may comprise a bead; that is, there may be some sites on the substrate surface which are empty. In addition, there may be some sites that contain more than one bead, although this is not preferred.

In some embodiments, for example when chemical attachment is done, it is possible to attach the beads in a non-random or ordered way. For example, using photoactivatible attachment linkers or photoactivatible adhesives or masks, selected sites on the array may be sequentially rendered suitable for attachment, such that defined populations of beads are laid down.

The arrays of the present invention are constructed such that information about the identity of the

capture probe is built into the array, such that the random deposition of the beads in the fiber wells can be "decoded" to allow identification of the capture probe at all positions. This may be done in a variety of ways, and either before, during or after the use of the array to detect target molecules.

Thus, after the array is made, it is "decoded" in order to identify the location of one or more of the capture probes, i.e. each subpopulation of beads, on the substrate surface.

In a preferred embodiment, pyrosequencing techniques are used to decode the array, as is generally described in "Nucleic Acid Sequencing using Microsphere Arrays", filed October 22, 1999 (no U.S.S.N. received yet), hereby incorporated by reference.

In a preferred embodiment, a selective decoding system is used. In this case, only those microspheres exhibiting a change in the optical signal as a result of the binding of a target sequence are decoded. This is commonly done when the number of "hits", i.e. the number of sites to decode, is generally low. That is, the array is first scanned under experimental conditions in the absence of the target sequences. The sample containing the target sequences is added, and only those locations exhibiting a change in the optical signal are decoded. For example, the beads at either the positive or negative signal locations may be either selectively tagged or released from the array (for example through the use of photocleavable linkers), and subsequently sorted or enriched in a fluorescence-activated cell sorter (FACS). That is, either all the negative beads are released, and then the positive beads are either released or analyzed in situ, or alternatively all the positives are released and analyzed. Alternatively, the labels may comprise halogenated aromatic compounds, and detection of the label is done using for example gas chromatography, chemical tags, isotopic tags mass spectral tags.

As will be appreciated by those in the art, this may also be done in systems where the array is not decoded; i.e. there need not ever be a correlation of bead composition with location. In this embodiment, the beads are loaded on the array, and the assay is run. The "positives", i.e. those beads displaying a change in the optical signal as is more fully outlined below, are then "marked" to distinguish or separate them from the "negative" beads. This can be done in several ways, preferably using fiber optic arrays. In a preferred embodiment, each bead contains a fluorescent dye. After the assay and the identification of the "positives" or "active beads", light is shown down either only the positive fibers or only the negative fibers, generally in the presence of a light-activated reagent (typically dissolved oxygen). In the former case, all the active beads are photobleached. Thus, upon non-selective release of all the beads with subsequent sorting, for example using a fluorescence activated cell sorter (FACS) machine, the non-fluorescent active beads can be sorted from the fluorescent negative beads. Alternatively, when light is shown down the negative fibers, all the negatives are non-fluorescent and the the postives are fluorescent, and sorting can proceed. The characterization of the attached capture probe may be done directly, for example using mass

spectroscopy.

Alternatively, the identification may occur through the use of identifier moieties ("IMs"), which are similar to IBLs but need not necessarily bind to DBLs. That is, rather than elucidate the structure of the capture probe directly, the composition of the IMs may serve as the identifier. Thus, for example, a specific combination of IMs can serve to code the bead, and be used to identify the agent on the bead upon release from the bead followed by subsequent analysis, for example using a gas chromatograph or mass spectroscope.

Alternatively, rather than having each bead contain a fluorescent dye, each bead comprises a non-fluorescent precursor to a fluorescent dye. For example, using photocleavable protecting groups, such as certain ortho-nitrobenzyl groups, on a fluorescent molecule, photoactivation of the fluorochrome can be done. After the assay, light is shown down again either the "positive" or the "negative" fibers, to distinquish these populations. The illuminated precursors are then chemically converted to a fluorescent dye. All the beads are then released from the array, with sorting, to form populations of fluorescent and non-fluorescent beads (either the positives and the negatives or vice versa).

In an alternate preferred embodiment, the sites of attachment of the beads (for example the wells) include a photopolymerizable reagent, or the photopolymerizable agent is added to the assembled array. After the test assay is run, light is shown down again either the "positive" or the "negative" fibers, to distinquish these populations. As a result of the irradiation, either all the positives or all the negatives are polymerized and trapped or bound to the sites, while the other population of beads can be released from the array.

In a preferred embodiment, the location of every capture probe is determined using decoder binding ligands (DBLs). As outlined above, DBLs are binding ligands that will either bind to identifier binding ligands, if present, or to the capture probes themselves, preferably when the capture probe is a nucleic acid or protein.

In a preferred embodiment, as outlined above, the DBL binds to the IBL.

In a preferred embodiment, the capture probes are single-stranded nucleic acids and the DBL is a substantially complementary single-stranded nucleic acid that binds (hybridizes) to the capture probe, termed a decoder probe herein. A decoder probe that is substantially complementary to each candidate probe is made and used to decode the array. In this embodiment, the candidate probes and the decoder probes should be of sufficient length (and the decoding step run under suitable conditions) to allow specificity; i.e. each candidate probe binds to its corresponding decoder probe with sufficient specificity to allow the distinction of each candidate probe.

In a preferred embodiment, the DBLs are either directly or indirectly labeled. In a preferred embodiment, the DBL is directly labeled, that is, the DBL comprises a label. In an alternate embodiment, the DBL is indirectly labeled; that is, a labeling binding ligand (LBL) that will bind to the DBL is used. In this embodiment, the labeling binding ligand-DBL pair can be as described above for IBL-DBL pairs.

Accordingly, the identification of the location of the individual beads (or subpopulations of beads) is done using one or more decoding steps comprising a binding between the labeled DBL and either the IBL or the capture probe (i.e. a hybridization between the candidate probe and the decoder probe when the capture probe is a nucleic acid). After decoding, the DBLs can be removed and the array can be used; however, in some circumstances, for example when the DBL binds to an IBL and not to the capture probe, the removal of the DBL is not required (although it may be desirable in some circumstances). In addition, as outlined herein, decoding may be done either before the array is used to in an assay, during the assay, or after the assay.

In one embodiment, a single decoding step is done. In this embodiment, each DBL is labeled with a unique label, such that the the number of unique tags is equal to or greater than the number of capture probes (although in some cases, "reuse" of the unique labels can be done, as described herein; similarly, minor variants of candidate probes can share the same decoder, if the variants are encoded in another dimension, i.e. in the bead size or label). For each capture probe or IBL, a DBL is made that will specifically bind to it and contains a unique tag, for example one or more fluorochromes. Thus, the identity of each DBL, both its composition (i.e. its sequence when it is a nucleic acid) and its label, is known. Then, by adding the DBLs to the array containing the capture probes under conditions which allow the formation of complexes (termed hybridization complexes when the components are nucleic acids) between the DBLs and either the capture probes or the IBLs, the location of each DBL can be elucidated. This allows the identification of the location of each capture probe; the random array has been decoded. The DBLs can then be removed, if necessary, and the target sample applied.

In a preferred embodiment, the number of unique labels is less than the number of unique capture probes, and thus a sequential series of decoding steps are used. In this embodiment, decoder probes are divided into n sets for decoding. The number of sets corresponds to the number of unique tags. Each decoder probe is labeled in n separate reactions with n distinct tags. All the decoder probes share the same n tags. The decoder probes are pooled so that each pool contains only one of the n tag versions of each decoder, and no two decoder probes have the same sequence of tags across all the pools. The number of pools required for this to be true is determined by the number of decoder probes and the n. Hybridization of each pool to the array generates a signal at every address. The sequential hybridization of each pool in turn will generate a unique, sequence-specific code for each candidate probe. This identifies the candidate probe at each address in the array. For example, if four

tags are used, then 4 X n sequential hybridizations can ideally distinguish 4^n sequences, although in some cases more steps may be required. After the hybridization of each pool, the hybrids are denatured and the decoder probes removed, so that the probes are rendered single-stranded for the next hybridization (although it is also possible to hybridize limiting amounts of target so that the available probe is not saturated. Sequential hybridizations can be carried out and analyzed by subtracting pre-existing signal from the previous hybridization).

An example is illustrative. Assuming an array of 16 probe nucleic acids (numbers 1-16), and four unique tags (four different fluors, for example; labels A-D). Decoder probes 1-16 are made that correspond to the probes on the beads. The first step is to label decoder probes 1-4 with tag A, decoder probes 5-8 with tag B, decoder probes 9-12 with tag C, and decoder probes 13-16 with tag D. The probes are mixed and the pool is contacted with the array containing the beads with the attached candidate probes. The location of each tag (and thus each decoder and candidate probe pair) is then determined. The first set of decoder probes are then removed. A second set is added, but this time, decoder probes 1, 5, 9 and 13 are labeled with tag A, decoder probes 2, 6, 10 and 14 are labeled with tag B, decoder probes 3, 7, 11 and 15 are labeled with tag C, and decoder probes 4, 8, 12 and 16 are labeled with tag D. Thus, those beads that contained tag A in both decoding steps contain candidate probe 1; tag A in the first decoding step and tag B in the second decoding step contain candidate probe 2; tag A in the first decoding step and tag C in the second step contain candidate probe 3; etc. In one embodiment, the decoder probes are labeled in situ; that is, they need not be labeled prior to the decoding reaction. In this embodiment, the incoming decoder probe is shorter than the candidate probe, creating a 5' "overhang" on the decoding probe. The addition of labeled ddNTPs (each labeled with a unique tag) and a polymerase will allow the addition of the tags in a sequence specific manner, thus creating a sequence-specific pattern of signals. Similarly, other modifications can be done, including ligation, etc.

In addition, since the size of the array will be set by the number of unique decoding binding ligands, it is possible to "reuse" a set of unique DBLs to allow for a greater number of test sites. This may be done in several ways; for example, by using some subpopulations that comprise optical signatures. Similarly, the use of a positional coding scheme within an array; different sub-bundles may reuse the set of DBLs. Similarly, one embodiment utilizes bead size as a coding modality, thus allowing the reuse of the set of unique DBLs for each bead size. Alternatively, sequential partial loading of arrays with beads can also allow the reuse of DBLs. Furthermore, "code sharing" can occur as well.

In a preferred embodiment, the DBLs may be reused by having some subpopulations of beads comprise optical signatures. In a preferred embodiment, the optical signature is generally a mixture of reporter dyes, preferably flourescent. By varying both the composition of the mixture (i.e. the ratio of one dye to another) and the concentration of the dye (leading to differences in signal intensity), matrices of unique optical signatures may be generated. This may be done by covalently attaching the

dyes to the surface of the beads, or alternatively, by entrapping the dye within the bead.

In a preferred embodiment, the encoding can be accomplished in a ratio of at least two dyes, although more encoding dimensions may be added in the size of the beads, for example. In addition, the labels are distinguishable from one another; thus two different labels may comprise different molecules (i.e. two different fluors) or, alternatively, one label at two different concentrations or intensity.

In a preferred embodiment, the dyes are covalently attached to the surface of the beads. This may be done as is generally outlined for the attachment of the capture probes, using functional groups on the surface of the beads. As will be appreciated by those in the art, these attachments are done to minimize the effect on the dye.

In a preferred embodiment, the dyes are non-covalently associated with the beads, generally by entrapping the dyes in the pores of the beads.

Additionally, encoding in the ratios of the two or more dyes, rather than single dye concentrations, is preferred since it provides insensitivity to the intensity of light used to interrogate the reporter dye's signature and detector sensitivity.

In a preferred embodiment, a spatial or positional coding system is done. In this embodiment, there are sub-bundles or subarrays (i.e. portions of the total array) that are utilized. By analogy with the telephone system, each subarray is an "area code", that can have the same tags (i.e. telephone numbers) of other subarrays, that are separated by virtue of the location of the subarray. Thus, for example, the same unique tags can be reused from bundle to bundle. Thus, the use of 50 unique tags in combination with 100 different subarrays can form an array of 5000 different capture probes. In this embodiment, it becomes important to be able to identify one bundle from another; in general, this is done either manually or through the use of marker beads, i.e. beads containing unique tags for each subarray.

In alternative embodiments, additional encoding parameters can be added, such as microsphere size. For example, the use of different size beads may also allow the reuse of sets of DBLs; that is, it is possible to use microspheres of different sizes to expand the encoding dimensions of the microspheres. Optical fiber arrays can be fabricated containing pixels with different fiber diameters or cross-sections; alternatively, two or more fiber optic bundles, each with different cross-sections of the individual fibers, can be added together to form a larger bundle; or, fiber optic bundles with fiber of the same size cross-sections can be used, but just with different sized beads. With different diameters, the largest wells can be filled with the largest microspheres and then moving onto progressively smaller microspheres in the smaller wells until all size wells are then filled. In this manner, the same dye ratio could be used to encode microspheres of different sizes thereby expanding the number of

different oligonucleotide sequences or chemical functionalities present in the array. Although outlined for fiber optic substrates, this as well as the other methods outlined herein can be used with other substrates and with other attachment modalities as well.

In a preferred embodiment, the coding and decoding is accomplished by sequential loading of the microspheres into the array. As outlined above for spatial coding, in this embodiment, the optical signatures can be "reused". In this embodiment, the library of microspheres each comprising a different capture probe (or the subpopulations each comprise a different capture probe), is divided into a plurality of sublibraries; for example, depending on the size of the desired array and the number of unique tags, 10 sublibraries each comprising roughly 10% of the total library may be made, with each sublibrary comprising roughly the same unique tags. Then, the first sublibrary is added to the fiber optic bundle comprising the wells, and the location of each capture probe is determined, generally through the use of DBLs. The second sublibrary is then added, and the location of each capture probe is again determined. The signal in this case will comprise the signal from the "first" DBL and the "second" DBL; by comparing the two matrices the location of each bead in each sublibrary can be determined. Similarly, adding the third, fourth, etc. sublibraries sequentially will allow the array to be filled.

In a preferred embodiment, codes can be "shared" in several ways. In a first embodiment, a single code (i.e. IBL/DBL pair) can be assigned to two or more agents if the target sequences different sufficiently in their binding strengths. For example, two nucleic acid probes used in an mRNA quantitation assay can share the same code if the ranges of their hybridization signal intensities do not overlap. This can occur, for example, when one of the target sequences is always present at a much higher concentration than the other. Alternatively, the two target sequences might always be present at a similar concentration, but differ in hybridization efficiency.

Alternatively, a single code can be assigned to multiple agents if the agents are functionally equivalent. For example, if a set of oligonucleotide probes are designed with the common purpose of detecting the presence of a particular gene, then the probes are functionally equivalent, even though they may differ in sequence. Similarly, an array of this type could be used to detect homologs of known genes. In this embodiment, each gene is represented by a heterologous set of probes, hybridizing to different regions of the gene (and therefore differing in sequence). The set of probes share a common code. If a homolog is present, it might hybridize to some but not all of the probes. The level of homology might be indicated by the fraction of probes hybridizing, as well as the average hybridization intensity. Similarly, multiple antibodies to the same protein could all share the same code.

In a preferred embodiment, decoding of self-assembled random arrays is done on the bases of pH titration. In this embodiment, in addition to capture probes, the beads comprise optical signatures, wherein the optical signatures are generated by the use of pH-responsive dyes (sometimes referred to

herein as "ph dyes") such as fluorophores. This embodiment is similar to that outlined in PCT US98/05025 and U.S.S.N. 09/151,877, both of which are expressly incorporated by reference, except that the dyes used in the present ivention exhibits changes in fluorescence intensity (or other properties) when the solution pH is adjusted from below the pKa to above the pKa (or vice versa). In a preferred embodiment, a set of pH dyes are used, each with a different pKa, preferably separated by at least 0.5 pH units. Preferred embodiments utilize a pH dye set of pKa's of 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11, and 11.5. Each bead can contain any subset of the pH dyes, and in this way a unique code for the capture probe is generated. Thus, the decoding of an array is achieved by titrating the array from pH 1 to pH 13, and measuring the fluorescence signal from each bead as a function of solution pH.

Thus, the present invention provides array compositions comprising a substrate with a surface comprising discrete sites. A population of microspheres is distributed on the sites, and the population comprises at least a first and a second subpopulation. Each subpopulation comprises a capture probe, and, in addition, at least one optical dye with a given pKa. The pKas of the different optical dyes are different.

In a preferred embodiment, "random" decoding probes can be made. By sequential hybridizations or the use of multiple labels, as is outlined above, a unique hybridization pattern can be generated for each sensor element. This allows all the beads representing a given clone to be identified as belonging to the same group. In general, this is done by using random or partially degenerate decoding probes, that bind in a sequence-dependent but not highly sequence-specific manner. The process can be repeated a number of times, each time using a different labeling entity, to generate a different pattern of singals based on quasi-specific interactions. In this way, a unique optical signature is eventually built up for each sensor element. By applying pattern recognition or clustering algorithms to the optical signatures, the beads can be grouped into sets that share the same signature (i.e. carry the same probes).

In order to identify the actual sequence of the clone itself, additional procedures are required; for example, direct sequencing can be done, or an ordered array containing the clones, such as a spotted cDNA array, to generate a "key" that links a hybridization pattern to a specific clone.

Alternatively, clone arrays can be decoded using binary decoding with vector tags. For example, partially randomized oligos are cloned into a nucleic acid vector (e.g. plasmid, phage, etc.). Each oligonucleotide sequence consists of a subset of a limited set of sequences. For example, if the limites set comprises 10 sequences, each oligonucleotide may have some subset (or all of the 10) sequences. Thus each of the 10 sequences can be present or absent in the oligonucleotide. Therefore, there are 2^{10} or 1,024 possible combinations. The sequences may overlap, and minor variants can also be represented (e.g. A, C, T and G substitutions) to increase the number of possible

combinations. A nucleic acid library is cloned into a vector containing the random code sequences. Alternatively, other methods such as PCR can be used to add the tags. In this way it is possible to use a small number of oligo decoding probes to decode an array of clones.

As will be appreciated by those in the art, the systems of the invention may take on a large number of different configurations, as is generally depicted in the Figures. In general, there are three types of systems that can be used: (1) "non-sandwich" systems (also referred to herein as "direct" detection) in which the target sequence itself is labeled with detectable labels (again, either because the primers comprise labels or due to the incorporation of labels into the newly synthesized strand); (2) systems in which label probes directly bind to the target analytes; and (3) systems in which label probes are indirectly bound to the target sequences, for example through the use of amplifier probes.

Detection of the reactions of the invention, including the direct detection of products and indirect detection utilizing label probes (i.e. sandwich assays), is preferably done by detecting assay complexes comprising detectable labels, which can be attached to the assay complex in a variety of ways.

In a preferred embodiment, an array of different and usually artificial capture probes are made; that is, the capture probes do not have complementarity to known target sequences. The adapter sequences can then be added to any target sequences, or soluble capture extender probes are made; this allows the manufacture of only one kind of array, with the user able to customize the array through the use of adapter sequences or capture extender probes. This then allows the generation of customized soluble probes, which as will be appreciated by those in the art is generally simpler and less costly.

When capture extender probes are used, in one embodiment, microsphere arrays containing a single type of capture probe are made; in this embodiment, the capture extender probes are added to the beads prior to loading on the array. The capture extender probes may be additionally fixed or crosslinked, as necessary.

Accordingly, the present invention provides compositions and methods for detecting the presence or absence of target analytes, including nucleic acid sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples (i.e. in the case of nucleic acids, the sample may be the products of an amplification reaction, including both target and signal amplification); purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the

art, virtually any experimental manipulation may have been done on the sample.

The present invention provides compositions and methods for detecting the presence or absence of target nucleic acid sequences in a sample.

In a preferred embodiment, several levels of redundancy are built into the arrays of the invention. Building redundancy into an array gives several significant advantages, including the ability to make quantitative estimates of confidence about the data and signficant increases in sensitivity. Thus, preferred embodiments utilize array redundancy. As will be appreciated by those in the art, there are at least two types of redundancy that can be built into an array: the use of multiple identical sensor elements (termed herein "sensor redundancy"), and the use of multiple sensor elements directed to the same target analyte, but comprising different chemical functionalities (termed herein "target redundancy"). For example, for the detection of nucleic acids, sensor redundancy utilizes of a plurality of sensor elements such as beads comprising identical binding ligands such as probes. Target redundancy utilizes sensor elements with different probes to the same target: one probe may span the first 25 bases of the target, a second probe may span the second 25 bases of the target, etc. By building in either or both of these types of redundancy into an array, significant benefits are obtained. For example, a variety of statistical mathematical analyses may be done.

In addition, while this is generally described herein for bead arrays, as will be appreciated by those in the art, this techniques can be used for any type of arrays designed to detect target analytes. Furthermore, while these techniques are generally described for nucleic acid systems, these techniques are useful in the detection of other binding ligand/target analyte systems as well.

In a preferred embodiment, sensor redundancy is used. In this embodiment, a plurality of sensor elements, e.g. beads, comprising identical bioactive agents are used. That is, each subpopulation comprises a plurality of beads comprising identical bioactive agents (e.g. binding ligands). By using a number of identical sensor elements for a given array, the optical signal from each sensor element can be combined and any number of statistical analyses run, as outlined below. This can be done for a variety of reasons. For example, in time varying measurements, redundancy can significantly reduce the noise in the system. For non-time based measurements, redundancy can significantly increase the confidence of the data.

In a preferred embodiment, a plurality of identical sensor elements are used. As will be appreciated by those in the art, the number of identical sensor elements will vary with the application and use of the sensor array. In general, anywhere from 2 to thousands may be used, with from 2 to 100 being preferred, 2 to 50 being particularly preferred and from 5 to 20 being especially preferred. In general, preliminary results indicate that roughly 10 beads gives a sufficient advantage, although for some applications, more identical sensor elements can be used.

Once obtained, the optical response signals from a plurality of sensor beads within each bead subpopulation can be manipulated and analyzed in a wide variety of ways, including baseline adjustment, averaging, standard deviation analysis, distribution and cluster analysis, confidence interval analysis, mean testing, etc.

In a preferred embodiment, the first manipulation of the optical response signals is an optional baseline adjustment. In a typical procedure, the standardized optical responses are adjusted to start at a value of 0.0 by subtracting the integer 1.0 from all data points. Doing this allows the baseline-loop data to remain at zero even when summed together and the random response signal noise is canceled out. When the sample is a fluid, the fluid pulse-loop temporal region, however, frequently exhibits a characteristic change in response, either positive, negative or neutral, prior to the sample pulse and often requires a baseline adjustment to overcome noise associated with drift in the first few data points due to charge buildup in the CCD camera. If no drift is present, typically the baseline from the first data point for each bead sensor is subtracted from all the response data for the same bead. If drift is observed, the average baseline from the first ten data points for each bead sensor is substracted from the all the response data for the same bead. By applying this baseline adjustment, when multiple bead responses are added together they can be amplified while the baseline remains at zero. Since all beads respond at the same time to the sample (e.g. the sample pulse), they all see the pulse at the exact same time and there is no registering or adjusting needed for overlaying their responses. In addition, other types of baseline adjustment may be done, depending on the requirements and output of the system used.

Once the baseline has been adjusted, a number of possible statistical analyses may be run to generate known statistical parameters. Analyses based on redundancy are known and generally described in texts such as Freund and Walpole, Mathematical Statistics, Prentice Hall, Inc. New Jersey, 1980, hereby incorporated by reference in its entirety.

In a preferred embodiment, signal summing is done by simply adding the intensity values of all responses at each time point, generating a new temporal response comprised of the sum of all bead responses. These values can be baseline-adjusted or raw. As for all the analyses described herein, signal summing can be performed in real time or during post-data acquisition data reduction and analysis. In one embodiment, signal summing is performed with a commercial spreadsheet program (Excel, Microsoft, Redmond, WA) after optical response data is collected.

Methods for signal summing and analyses are included in U.S.S.N. 08/944,850, filed October 6, 1997; 09/287,573, filed April 6, 1999; and 60/238,866, filed October 6, 2000; an PCT Nos. US98/21193, filed October 6, 1998; and US00/09183, filed April 6, 2000.

Once made, the methods and compositions of the invention find use in a number of applications. In a

preferred embodiment, the compositions are used to probe a sample solution for the presence or absence of a target sequence, including the quantification of the amount of target sequence present. The compositions and methods find utility in the detection of genotyping assays and sequencing assays, and in all sorts of target analyte assays, including immunoassays.

For SNP analysis, the ratio of different labels at a particular location on the array indicates the homozygosity or heterozygosity of the target sample, assuming the same concentration of each readout probe is used. Thus, for example, assuming a first readout probe comprising a first base at the readout position with a first detectable label and a second readout probe comprising a second base at the readout position with a second detectable label, equal signals (roughly 1:1 (taking into account the different signal intensities of the different labels, different hybridization efficiencies, and other reasons)) of the first and second labels indicates a heterozygote. The absence of a signal from the first label (or a ratio of approximately 0:1) indicates a homozygote of the second detection base; the absence of a signal from the second label (or a ratio of approximately 1:0) indicates a homozygote for the first detection base. As is appreciated by those in the art, the actual ratios for any particular system are generally determined empirically.

Generally, a sample containing a target analyte (whether for detection of the target analyte or screening for binding partners of the target analyte) is added to the array, under conditions suitable for binding of the target analyte to at least one of the capture probes, i.e. generally physiological conditions. The presence or absence of the target analyte is then detected. As will be appreciated by those in the art, this may be done in a variety of ways, generally through the use of a change in an optical signal. This change can occur via many different mechanisms. A few examples include the binding of a dye-tagged analyte to the bead, the production of a dye species on or near the beads, the destruction of an existing dye species, a change in the optical signature upon analyte interaction with dye on bead, or any other optical interrogatable event.

In a preferred embodiment, the change in optical signal occurs as a result of the binding of a target analyte that is labeled, either directly or indirectly, with a detectable label, preferably an optical label such as a fluorochrome. Thus, for example, when a proteinaceous target analyte is used, it may be either directly labeled with a fluor, or indirectly, for example through the use of a labeled antibody. Similarly, nucleic acids are easily labeled with fluorochromes, for example during PCR amplification as is known in the art. Alternatively, upon binding of the target sequences, a hybridization indicator may be used as the label. Hybridization indicators preferentially associate with double stranded nucleic acid, usually reversibly. Hybridization indicators include intercalators and minor and/or major groove binding moieties. In a preferred embodiment, intercalators may be used; since intercalation generally only occurs in the presence of double stranded nucleic acid, only in the presence of target hybridization will the label light up. Thus, upon binding of the target analyte to a capture probe, there is a new optical signal generated at that site, which then may be detected.

Alternatively, in some cases, as discussed above, the target analyte such as an enzyme generates a species that is either directly or indirectly optical detectable.

Furthermore, in some embodiments, a change in the optical signature may be the basis of the optical signal. For example, the interaction of some chemical target analytes with some fluorescent dyes on the beads may alter the optical signature, thus generating a different optical signal.

As will be appreciated by those in the art, in some embodiments, the presence or absence of the target analyte may be done using changes in other optical or non-optical signals, including, but not limited to, surface enhanced Raman spectroscopy, surface plasmon resonance, radioactivity, etc.

The assays may be run under a variety of experimental conditions, as will be appreciated by those in the art. A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding. Various blocking and washing steps may be utilized as is known in the art.

The following examples serve to more fully describe the manner of using the above-described invention, as well as to set forth the best modes contemplated for carrying out various aspects of the invention. It is understood that these examples in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references cited herein are incorporated by reference in their entirety.

Examples

Example 1

Immobilization of Crude Oligonucleotides to a Solid Support

1. Introduce chemical functional group (such as -NH2, -COOH, -NCO, -NHS, -SH, -CHO, etc.)onto solid support.

2. Activate the functional group before oligonucleotide attachment.

3. 5'-terminal modified oligonucleotide attachment.

Crude Oligonucleotides were attached to supports and compared to results from attachment of purified oligonucleotides. As demonstrated in Figure 3, in the presence of 2M salt, crude oligonucleotides were immobilized as efficiently as purified oligonucleotides.

IN addition, the improved attachment of oligonucleotides to a solid support in the presence of increased salt was sequence and length independent. Thus, the method finds use in attachment of all oligonucleotides to a solid support (see Figure 4).

In addition, when 0.5 M to 3 M NaCl was used for attachment of oligonucleotides, non-purified oligonucleotides were attached with comparable efficiency when compared to purified oligonucleotides (see Figure 5).

TABLE 1

Seq. ID No.	Decoder (5'-3')
17	GGCTGGTTCGGCCCGAAAGCTTAG
18	GTTCCCAGTGAAGCTGCGATCTGG
19	TACTTGGCATGGAATCCCTTACGC
20	ACTAGCATATTTCAGGGCACCGGC
21	GAACGGTCAATGAACCCGCTGTGA
22	GCGGCCTTGGTTCAATATGAATCG
23	GATCGTTAGAGGGACCTTGCCCGA
24	TGGACCTAGTCCGGCAGTGACGAA
25	ATAAACTACCCAGGACGGGCGGAA
26	CATCGGTTCGCGCCAATCCAGATA
27	GTCGGGCATAGAGCCGACCACCCT
28	CTTGGGTCATGATTCACCGTGCTA
29	TGCCTAACGTGCTAATCAGCAGCG
30	CGCATGTTGGAGCATATGCCCTGA
31	AGCCACTGCATCAGTGCTGTTCAA
32	GGTTGTTTTGAGGCGTCCCACACT
33	TCGACCAAGAGCAAGGGCGGACCA
34	GACATCGCTATTGCGCATGGATCA
35	GAAATACGAAGTCTGCGGGAGTCG
36	TGTCATGAATGATTGATCGCGCGA
37	ATATCGGGATTCGTTCCCGGTGAA
38	GCGAGCGTACCGAAGGGCCTAGAA
39	TTACCGGCAGCGGACTTCCGAATT
40	GTAATCGAGAGCTGCGCGCCGTCT
41	TCCCTGAGGTCGGAAGCTTCCGAC
42	CCTGTTAGCGTAGGCGAGTCGATC
43	TAGCGGACCGGCAGAATGAGTTCC
44	GGTACATGCACTACGCGCACTCGG
45	AATTCATCTCGGACTCCCGCGGTA
46	GCCAAATCTGGATTGGCAGGAATG
47	TGCATTTTCGGTTGAGGCACATCC
48	CCGCTCAATTCACCATGCTTCGCT
49	CTCGGAAAGGTGCAACTTTGGTGT
50	AATTCGACCAGCAGAACGTCCCAT
51	GCCAGAGTCTCAACCTCACGGGAT
52	CCAACAACTGGAACGGGAACCCGC
53	GAGAACTGATCGCTGAGGGGCATG
54	GGCACACTAGACTTGTGGCACCGA

55	CTTGGGCAAACGCTTCAGCCACAA
56	TCACATCCAAATATGGTCCGCGAA
57	GTCTGCCGGTGTGACCGCTTCATT
58	CATCGCAGAGCATAAACACCCTCA
59	GTTGGTATCTATGGCAGAGGCGGA
60	ACGAGGTGCCGCTGAGGTTCCATT
61	GGAATGAGTGGACCCAGGCACATT
62	TGTCAATATGCGTCCGTGTCGTCT
63	TGATGAGCCTCAGGGTACGAGGCA
64	CACCGCGGTGTTCCTACAGAATGA
65	TTGTTGCCAATGGTGTCCGCTCGG
66	TTAACCTGCGTCTGCCCCTTTCCT
67	AGGCGCGTTCCTGCCTTAGTGACG
68	TAGGGCGATGGCACGAAGCTTCAA
69	TGCATAGAGCCAAAGTCGGCGATG
70	TTGAGAGGCAGGTGGCCACACGGA
71	TCCGCATTGTGAGAAAAAACGAGC
72	GGCGGTTTCCGTAGCTATAGGTGC
73	GGTGAAAATTTCGTAGCCACGGGC
74	CCGACGGAGGATGAAGACAATCAC
75	CCAGTTTGGCCCAATTCGCCAAAA
76	GGATCTATTAGGCCGTGCGCACAG
77	CGGATGTCACCGTTTGGACTTTCA
78	ATCGCAAATCCTGCTCGTCCCTAA
79	CAGGGCATGCAATAATCGAGGTTC
80	CATGCGTTGATATATGGGCCCAAG
81	CAGCTGCAGCTTGTGACCAACCAC
82	TTGTATGTCTGCCGACCGGCGACC
83	GATGGCGCCCGTTGATAGGTATGG
84	ATGAGAATCGCCGGCAATCTGCTA
85	ATTTGCACTGACCGCAGGCTCGTG
86	CAGGGAGAACGGTTAAGTTCCCGT
87	AGGCCGGCGATCGAGGAGTTTGGT
88	ACACGGTGGTCTCTGATAGCGACC
89	GTGCAACGCCGAGGACTTCCATCA
90	TCGGTGCCTGATAGCCATTCCGAT
91	TGAAATACCACACAGCCAATTGGC
92	GCATCGTGTACATGACTGCCGCGA
93	CAGTGTTCTAACGGCGCGCGTGAA
94	CGCTTGCAACGTTGCACCTACTCT
95	CGAAAAACTAGTGGGCTCGCCGCG
96	CTTTCAGGGGAACTGCCGGAGTCG

97	TTGTGGCCTTCTTGTAAAGGCACG
98	TCCACGAACGGCGACCCGTTGTCT
99	CGACCTTGCACGAAACCTAACGAG
100	GTGCAGCTTCACGAGCCAGCCTGA
101	CGCTTTCGTGCGAATAGACGATGA
102	TGCGCTTACAGGCTCCTAGTGGTC
103	CACGCGCTTAGTCGCGATCGCATA
104	CGGAGGGAGGGAGCTAGCCTTCGA
105	GCATCCGGCCTGTTGATGACGCCT
106	AGGCCAATCGATCTTATTGCCGAG
107	CCTTCCAATGATTGCATACGCCCA
108	AACACTTGATCAGGCGGGTCGTCT
109	TGGAATCAAGGCCGTAAAGGACAG
110	GCTCCCGTAACCTGTCCACCAGTG
111	AGTGGTGAATGGCCGCTACCCTGA
112	TGTTGAAGCGAGCTAAAACGGCCA
113	CAGCGCTCCAGAATTGACAGCAAT
114	AAGGTGGTGCCATTCATTTGGCTA
115	CGTTAAACCGCAATCCGTTCGGCT
116	TGTCTTCCACCTCGAAGGTTTCCA
117	CACGAGATACCGGCGTAAGGGTGG
118	CTACGGCAAACGTGTGGAATGGGT
119	GTAGGGCGATGACGGGCGAACTAC
120	AATCGACCTCCGCACACATTCGCA
121	GAGTCAGCATGGCGGCGGAGATTC
122	AGATAAAGACGCTGGCAACACGGG
123	GGTACCTCAACGCGAACCACTTGT
124	AAGCGATGGCTACCCAAGAGCGAT
125	AGAGCTTATGCAGAACCAGGCGCC
126	ATCGGTCTCACGCAGGGTTGGATA
127	TAGGTTGCCCGCCAGAAGAAACAT
128	CGGTGCTGTTGCAAAAGCCTGTAG
129	TGATGAAAGTTTGCGGCAGGACAC
130	GTTGAGTGCAGGATGCAGCGATAG
131	AACATTGCGCGGTCCACCAGGGTT
132	GGGCAGTTAGAGAGGGCCAGAAGT
133	TCGAGCTGGTCCCCGTGAACGTGT
134	GTCTTGGGGGCCGCTTAGTGAAAA
135	ACTGTTGGCTTGCTCTCATGTCCA
136	AGGACCATTCGGAAGGCGAAGATA
137	CTTGGGAGGCATCCGCTATAAGGA
138	AATAAACGGAACGCACCGCTACAG

139	TTGTACGTGCGGTCCCCATAAGCA
140	CGCACCAAACTGAGTTTCCCAGAC
141	ACCTGATCGTTCCCCTATTGGGAA
142	GGAACAGAGGCGAGGGGACTGAGC
143	CCCTGCCTTGGCGTGTCGGCTTAT
144	ACTCTGACACGCCAACTCCGGAAG
145	CTGACGGTTTTCATTCGGCGTGCC
146	TGCGGTGGTTCATTGGAGCTGGCC
147	GCATGGCCAACTAGTGACTCGCAA
148	AGGCCGTAAAGCGAATCTCACCTG
149	CGAATATTATGCCGAGAATCCGCG
150	ACAGACGAGCTCCCAACCACATGA
151	GGACGGTTTGTGCTGGATTGTCTG
152	AAAGGCTATTGAGTTGGTTGGGCG
153	GATGGCCTATTCGGAGATCGGGCC
154	GATCCAGTAGGCAGCTTCATCCCA
155	AATAACTCGCGCGGGTATGCTTCT
156	GGAGGAGGTTTGTCTCGGAAAGCA
157	CTTTGGTATGGCACATGCTGCCCG
158	AGAAAGGCTCGAGCAACGGGAACT
159	AATCTACCGCACTGGTCCGCAAGT
160	CGTGGCGGCCACAGTTTTTGGAGG
161	TTGCAGTTCAATCCATACGCACGT
162	GGCCCAAAGCCCCAGACCATTTTA
163	CGCCTGTCTTTGTCTCCGGACAAT
164	TGAGGCAACAGGGGCCAAAAACTA
165	AGCGGAAGTAGTCCTCGGCTCGTC
166	GGCCCCAAGGCTTAGAGATAGTGG
167	GCACGTGAAGTTTAACCGCGATTC
168	AGCGGCAGAAACGTTCCTTGACGG
169	TCGTCGAGCAGACGAGATTGCACG
170	TCTTTGCCGCGTAACTGACTGCTT
171	TTTATGTGCCAAGGGGTTAACCGA
172	TGTTACTGTGGTTCACGGCAGTCC
173	CGCGCCTCGCTAGACCTTTTATTG
174	ACAAATGCGTGAGAGCTCCCAACT
175	CGCGCAGATTATAGACCCGAATGT
176	CAAATAACGCCGCTGAATCGGCGT
177	CCTTCGTGCATCGGTGATGATGTT
178	TGAACACGAGCAACACTCCAACGC
179	CAGCAGATCCTTCGTAGCGGTCGT
180	GGAACCTGGTGAGTTGTGCCTCAT

181	TCATAAGCGACAATCGCGGGCTTA
182	CCCAACGTCACTGAAGCTCACAGT
183	TGTCAGAGCCCGCGACTCAGACGG
184	TACACGAAGCCTCTCCGTGGTCCA
185	CTCAGAAGTCCTCGGCGAACTGGG
186	ATCCTTTTATCTACTCCGCGGCGA
187	AGGCGTGCAGCAACAGGATAAACC
188	ACTCTCGAGGGAGTCTCTGGCACA
189	TTGCCAGGTCCATCGAGACCTGTT
190	TCCACTATAACTGCGGGTCCGTGT
191	GCCCAGTCGGCTCTAACAAGTTCG
192	CGGAACGGATAATCGGCGTCAGGT
193	TAAAATAAGCGCCTGGCGGGAGGA
194	GCGCACTCGTGAAACCTTTCTCGC
195	AGTTTGCCAGGTACTGGCAAGTGC
196	ACAACGAGGGATGTCCAGCGGCAT
197	TTCGCAGCACCCGCTAGGTACAGT
198	TAACCCGATTTTTGCGACTCTGCC
199	CGTCGCATTGCAAGCGTAGGCTTG
200	GAGCTGACGTCACCATCAGAGGAA
201	GGAGGCTGGGGGTCGCGCTTAAGT
202	TTGTGGGAACCGCACTAGCTGGCT
203	CCCTCGCACTGTGTTCACCCTCTT
204	TCATTGACTCGAATCCGCACAACG
205	ACAGGGGTTGGCCTTCGTACGTAC
206	AGGCCGTGCAACATCACACAGGAT
207	GGGCCGTGGTCACGTAATATTGGC
208	GCGCGGACATGAAACGACAAGGCC
209	CTTATTGGGTGCCGGTGTCGGATT
210	GGGGCGGTTACCAAAAAATCCGAT
211	GCTAAAGCGTGCTCCGTAACTGCC
212	ATCTCATGCATCTCGGTTCGTCGT
213	ACGAAAAAAGTGTGCGGATCCCCT
214	CCAAGTACACCGCACGCATGTTTA
215	ATCGTGCGTGGAGTGTCGCATCTA
216	TCCAGATACCGCCCCGAACTTTGA
217	TCTGCTGGCAGCACGTGAAGTGGC
218	TTGAAATTGCTCTGCCGTCAGTCA
219	AGTCAGGCGAGATGTTCAGGCAGC
220	ACAAGCCGACGTTAAGCCCGCCCA
221	CCCTAATGAGGCCAGTAACCTGCA
222	GTGAGACACACATCCCCTCCAATG

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1792	CAGGGCGGTGCGGTGAACTAGCCA
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1795	AGCGGACACCTGTACTCTCCTCCA
1796	GGAGCCACACCAGTCGAAGATGGT
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1802	GCTGGGTATAGTTGCCTGGCAATG
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1829	GGGAGCTGGTGAGCAGATGTAACG
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3797	AAGCGGTTTGATCTGTGCAATCGG
3798	CTGTCAACTCGGTCGTCCGCACAG
3799	AACTTTGCCGTTTAGGGCAGGTGA
3800	GCTGAAGAACTCCCAATTCGCTGG
3801	AAGATGCGATGGGTCAGTCCTCGT
3802	ACCCACCTCTGAAGGTTGAGACGG
3803	AGGCTACGCACCCTCGAGAGTGAC
3804	CGGTCACGAACGTGGTCCAGTTTT
3805	CAAAGCAACGCGCGCCACTTAAAA
3806	ACGAGGAAGGAACTGATCCCCAGT
3807	TTCGCCACTATGGGCTCAGCATTA
3808	CGCTCGGCAGAGGAGTCCACTCAC
3809	TGTTGGCACGACTCCGTCCATGAA
3810	TGCCTACCCGGTGATTGCGACATC
3811	CAACGGTCGGATCTGAGGAGATCT
3812	CGTTACGAAGCGAAGTTCCCGAGT
3813	AGTGACGGCCAAAGTCGCCATTCT
3814	ATTCAGCTGGGCATAGGCGATGGG
3815	TAGGACAGCGTGGCTGGCTACACA
3816	AATTTGTCCAGCTCTGCACGACCG
3817	TGAGTGGGCTGTGATCCGTTCCAC
3818	TGTGGTGACACGCCAGAGCTGGTT
3819	CCTCACAGGTGTGAGAGGAGCCGC
3820	AGTCCCGCTTCTGCAAATTCCGAA
3821	TCTGCGCCTACCCGTAAGCTGAAC
3822	GCCTCCTGAGTTGATTCATGCATG
3823	CCTAACGGTTGGTTCGCCGTTTTT
3824	TCGCAAACCCACGAATGAGTCCCG
3825	AGTGCTAAGGTGGGCGAGCAGAGG
3826	CTGGAGACTGCGATGGCAGGGTTG
3827	AAGGGATAGTGATGGCGATGGACG
3828	CTATCCACGGTGATGTCCGCCATT
3829	CGGACTAGAACTTGCCAAGCACGA
3830	AGAGCCGGATGGCATTGCATGAAC
3831	AGTTGGCTAGCGGTCGAATGAGCA
3832	GCATGCGGTCACCGCTTCATCTAA
3833	GTGAGATTCCAAGCTCGCCGGTGA
3834	GCCATCCACCGCACAATGAACGCT

3835	GGGTGGTCCTCACTGTGGTTGGCA
3836	AGGCGGCTACGACGAGCGTCGTTA
3837	GCCAAGTGATCGTGCTTCCGCGTA
3838	TAGCCGTTTATTCCCTTGATGCGC
3839	ACTATGTGGGACGAGCGTCTGCGA
3840	GCACCTTCGAGAACCCATCAGATG
3841	ATTTTCTGTACCGATGCTCACCGG
3842	CACTGGAGCAATAAATGGCCAGGC
3843	GGGTTCACGTATCTCATGGATGCG
3844	GCACGCTCCCAGTATGCTCCTTCA
3845	GAAGGGACTTAGTCCGCGGCCCTC
3846	TTCGTTACCCTAAGGGCGTTTGCA
3847	GTTCCAGGTCACGACGAGCTGCGC
3848	TCGTACGTAGTCACACCGCGACTT
3849	GGGCTGGAGTAGCGGTCTGCTATG
3850	TAGCGGCACTCGTGTTGCGAGTGG
3851	ACGTTGGGTTCTGACACGGCGATT
3852	TGTTGCTGCGCCCCAAGTGATCTT
3853	CCCAGGTCGTTACGGTGCATCACA
3854	CCTAGTGCACAGGCAAATCGGGCT
3855	GGCGTTCTCCAAGATAAGGCCAAA
3856	ACTTCGATACCGTGGACCTCGCCA
3857	CTGAGCGCGCTAAACGTCCCTAGC
3858	ATCAGATAAACGATCCGACGCGTC
3859	CATGGCTGAATTTGTCGACCCTCT
3860	CGAAAGCGAGCAAATAGAATCCCC
3861	AGATTGCCCTGCGGCAGGTTGAAT
3862	AAGAGGCGGCCGATCAGTTAGAAA
3863	CTGATGCCTGTAAGGAGGCGCTCG
3864	AATCGCGAGGTTCGGCAGACAAAG
3865	CGTTGGGACACGGACCGTTCACTC
3866	AGATGTGTGCACTCGCGGTCATTT
3867	CAACTCGAGTGGCGGTAACATCTG
3868	ACCAAGGTTGCGATTACGGGAAGC
3869	CGAAGCGGTAGACGGCTCGCGTTA
3870	TCTCGCGAACAGGAGGGAAGGCGT
3871	GTCCCGATTTGCGCTGTGAGGAAA
3872	TACCACGCGTCGGCACGGAAATGG
3873	AAATGCTACCCGATTGCGCGGGAT
3874	TCGATTCAGGTTTGTGCTGCGGAG
3875	CCATCTCATCCCACTATGGCATGC
3876	CTGGCCCGTGTTTGGTTGAGTCGA

3877	GACACACACGTTGCAGGGCTTCCC
3878	TCGAATCGAGTCGATCGTGAAGGT
3879	GAAAGCACTCGATCGCGTTGGATT
3880	AATTACGCGAACATGGGGCGTCAA
3881	GTGCTAACACTGTGGTCGTTCCCA
3882	GGTAAGCGCCAGCCAGGAGTTGTC
3883	GGCGATCGTTCAGGAATCGCGTCA
3884	CTGGCTAGACCTCCGACACAGGCT
3885	CGGGTTAAACGCCAACTGGCCTAG
3886	ATCGCAGCCTGGCCGCCTAGTTTT
3887	GGCGTAGCCTAGCAAATTATGCCA
3888	ATGACGCGACGGAGACAATACGGC
3889	GTTGCATCACGAAAATGCCGTCTT
3890	GAGTCATGCGTTCCTCGCTTTACC
3891	TCTGAACCGGTTATCCCCAACCTC
3892	TGCCTCTGGTAGGCGCCCAGTTAC
3893	CTGACGGTTTTCATTCGGCGTGCC
3894	TGAACACGAGCAACACTCCAACGC
3895	CGGCGCGCGAAAGACTTGAACTTG
3896	GCTACGAGTACCCGTCGGAAACGC
3897	ATACCCAACAGCATGGAGCGACCA
3898	ATCGCATCGCATCGTATTCACGGG
3899	CGGCCTAGAGGTGCGAAAGCTATC
3900	TAACGCTTTTCCGAGGCCGATTCT
3901	TCTGTCCTAGCACGCCGACCTGCT
3902	CTCATCGTTCAGTCGGTCGTCGTA
3903	TCGTCGAGCAGATAGCGGGGTAGG
3904	TCGACCACAGTCAGGACACTACCG
3905	TGCGATTCTATGATGTCCGAACGC
3906	CAAATGCAATGGCAAGCACTCACC
3907	TCTAATCCATCGTTTTTTGGGCGA
3908	TCTCAACTCCGGTACGACGAAACA
3909	CTGAAGAGGGTAGCCTGGGAGCGG
3910	GGCACAATTAAAACGCGCCGCGTT
3911	CAAAGGAGGGTCAAAGGCCAGAAA
3912	TTTGCGGCCGTGACGAGCAAAAAT
3913	AGGAATGTGCGTGGCACCTGTGGA
3914	TCGTGATGACTGCCTTCCGAATCA
3915	CACGTCGACATGTTTGGTACCTCG
3916	TTGCGGTAGTTTGGTTACCACCGT
3917	GCAGTGGCGACAAATACAGCTGAG
3918	ACGGCATGATGGAGGGATAAACGT

3919	TGGGATAATCCGCAAGCGCATAGC
3920	CCTAGCTCTGCTGCGTCTTTGCGC
3921	TCCTGGAACTGCTGAAGGCGACTT
3922	CGAAGGCGGCATGGTGTAGTCTCC
3923	AACATTGTTCCCATCCCAGAGCAC
3924	CCAGGCAAGAAACAACCACGCGCT
3925	AAATCCACAGGCGCGCCAAAGCTG
3926	GCTCACCGCAGACTCCGCGCGATA
3927	TAGGTGGCGAGAGAGCGCCCACAA
3928	GGCGTTGGTGTGTCGGGACCATGA
3929	TCTGAATGCTTCCGTGCTTTCGTG
3930	ACGCTCTGGACCTCGCTCATTCGA
3931	TCCTTTATGCGCAGCGCTCGTGTT
3932	TTGCCGTCCTGCAGCAGGTAGCTC
3933	GGTCTAGTGGCAGCAAGGAGCGAT
3934	GGTAACGCGACCAGCTTAGACACC
3935	GTGGCGATTGGCTTCCTATGCATA
3936	TCAAAATACGGCCAGGAAGGGCAA
3937	TGCCATGCAGTCAGGTACGATGGT
3938	ACAGGTTACGTCGTGTGTTCCCGT
3939	CTCATGACGAACGAGCGGTCTGCA
3940	GTCGTGCGAGAGGCCAAGACCTTA
3941	GCTGGCTGACGCTGTTGTCAGAGG
3942	GCTACAGTGCTGCGTCCCGTGCCT
3943	TTTACGAGCACCAAGCTGGCGTAG
3944	ACGAGTTGACGGTCGTAGGGACCG
3945	TCGGATGGTAGGAGGCGAGATCGG
3946	ATTATGCAGATCCTGTGCATCCGC
3947	AGGGATGGAGACGAAGGAAGCATT
3948	ACCCCAGGACCCGTATTCCCTAGC
3949	GCACCATCCTGGGGCTTCTCAATG
3950	TACAATCCGTGGACGTTTGCTCAG
3951	GGTAGGCGAATCCGACTGGCATAG
3952	AGGACCGAACCCATGTGCAGCATC
3953	ATACACCGCACAGAAGCACAGCTG
3954	TCCTTGGCGGCCGTGTGTTTATTG
3955	CTCCACGCGAAGGGCGCTTGTAAC
3956	TGGCCCTGCCATCCTCGGATTCAG
3957	TGTCTATTCGCCAGCGTGAGCATC
3958	TGTTGTTGGCACGCCTCTACGGCA
3959	GTGCCTCAACCGTATCGTGGCGGT
3960	TCCTCGAAGTAGCGTGACCGAACC

3961	AAACAATTTCCTGCACTCTCGGCC
3962	CACAAACTCGTCGAGGCACACAGT
3963	GACGAAACGCTCGGCAGAAAGCCT
3964	TCAACTCACACGGGACAGCAGTTC
3965	TCACGTGGATGGGCTTAGCTGGGC
3966	AGGTGTTTGTTCCGACTGGCCACA
3967	TCAACCCTCTATTCCCGAGCATTG
3968	ACCTCACACAAGCGTTCTCGTCGA
3969	AACAGCATGCGGTCGCTGGCTTTC
3970	CACGGACACGTGTTACATCCGATG
3971	CTGGGAGCCTGCTGATACATGGTG
3972	CGTCCTATGGGCCATGGCCAGGAT
3973	GTCCCCAAATCTCGCTTTACAGGC
3974	TCACAAACCTGTGCGTGCATTGTC
3975	CACACTCGTGGCCTGCGTTGGGAA
3976	GCCTGCACTTACGGCTATCTCGCC
3977	TTGGCGTGGCGATTACCTGTTATT
3978	TTTGCGGCTGAAGTTTACAGGGTG
3979	CACTTAAGGGGCTGACCGAGCAAC
3980	AGAAAACGTCAATCCGCCACCTTT
3981	AACAAAACGGCGCTCCAACAAACG
3982	GCCTCAATATCTGGTTGCCGCCTG
3983	TTCCACAGTCAATGATGGGCGTGC
3984	GATTCCCAGTCTACCCGCGAGCAT
3985	AGGCCAATTACGACCCTGTCACGG
3986	CATGCGAACGTTCCGAGGAGACGG
3987	CACACGCGATGGGTTGTGTGACGC
3988	TCCGGTATTGCGCAGGAACCATAG
3989	AAGATTAGGTGTGCCCGCCTCAGG
3990	TCGTTACGCCCCGACTCGACGATG
3991	ACTAAAATCGCCAGGTTGCTCCCT
3992	AGGATGGCCACGCCGAATCAAAGT
3993	TGATGAAGCAGCTCATCGCTGGCG
3994	CCCCGATGGGTCTTTGTTGGACTC
3995	ACACGAGGGCTGCTGGTGAGGGCT
3996	TGGTCACCAATTTGATGATCCGAG
3997	AAGGCCGCTTGCATGCGACAAATT
3998	CCAGTGTTCGTTCATCGGTGGCGT
3999	CCGACCGCTACATAGGTGTGCGAA
4000	TGTTGAAGCCGTTCCCAGATGACA

TABLE 2

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1	TTCGCCGTCGTGTAGGCTTTTCAA	TTGAAAAGCCTACACGACGGCGAA
2	TTCGAAGCGCACGTCCCTTTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
3	AACGCGTGGGGAATGGGACATCAA	TTGATGTCCCATTCCCCACGCGTT
4	CCGTCGCATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
5	ATGGCCGTGCTGGGGACAAGTCAA	TTGACTTGTCCCCAGCACGGCCAT
6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCCGTTGCAA
7	CGCATAGGTTGCCGATTTCGTCAA	TTGACGAAATCGGCAACCTATGCG
8	CCGTTTGCGGTCGTCCTTGCTCAA	TTGAGCAAGGACGACCGCAAACGG
9	TTCGCTTTCGTGGCTGCACTTCAA	TTGAAGTGCAGCCACGAAAGCGAA
10	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCGCGTTGGAC
11	TTGCCGCACCGTCCGTCATCTCAA	TTGAGATGACGGACGGTGCGGCAA
12	CATCGTCCCTTTCGATGGGATCAA	TTGATCCCATCGAAAGGGACGATG
13	GCACGGGAGCTGACGACGTGTCAA	TTGACACGTCGTCAGCTCCCGTGC
14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
15	CGTGTAGGGGTCCCGTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
16	CATCGCTGCAAGTACCGCACTCAA	TTGAGTGCGGTACTTGCAGCGATG
17	GGCTGGTTCGGCCCGAAAGCTTAG	CTAAGCTTTCGGGCCGAACCAGCC
18	GTTCCCAGTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAC
19	TACTTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
20	ACTAGCATATTTCAGGGCACCGGC	GCCGGTGCCCTGAAATATGCTAGT
21	GAACGGTCAATGAACCCGCTGTGA	TCACAGCGGGTTCATTGACCGTTC
22	GCGGCCTTGGTTCAATATGAATCG	CGATTCATATTGAACCAAGGCCGC
23	GATCGTTAGAGGGACCTTGCCCGA	TCGGGCAAGGTCCCTCTAACGATC
24	TGGACCTAGTCCGGCAGTGACGAA	TTCGTCACTGCCGGACTAGGTCCA
25	ATAAACTACCCAGGACGGGCGGAA	TTCCGCCCGTCCTGGGTAGTTTAT
26	CATCGGTTCGCGCCAATCCAGATA	TATCTGGATTGGCGCGAACCGATG
27	GTCGGGCATAGAGCCGACCACCCT	AGGGTGGTCGGCTCTATGCCCGAC
28	CTTGGGTCATGATTCACCGTGCTA	TAGCACGGTGAATCATGACCCAAG
29	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
30	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
31	AGCCACTGCATCAGTGCTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
32	GGTTGTTTTGAGGCGTCCCACACT	AGTGTGGGACGCCTCAAAACAACC
33	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTTGCTCTTGGTCGA
34	GACATCGCTATTGCGCATGGATCA	TGATCCATGCGCAATAGCGATGTC
35	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCGCAGACTTCGTATTTC
36	TGTCATGAATGATTGATCGCGCGA	TCGCGCGATCAATCATTCATGACA
37	ATATCGGGATTCGTTCCCGGTGAA	TTCACCGGGAACGAATCCCGATAT

38	GCGAGCGTACCGAAGGGCCTAGAA	TTCTAGGCCCTTCGGTACGCTCGC
39	TTACCGGCAGCGGACTTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGCAGCTCTCGATTAC
41	CCTGTTAGCGTAGGCGAGTCGATC	GATCGACTCGCCTACGCTAACAGG
42	TAGCGGACCGGCAGAATGAGTTCC	GGAACTCATTCTGCCGGTCCGCTA
43	GGTACATGCACTACGCGCACTCGG	CCGAGTGCGCGTAGTGCATGTACC
44	AATTCATCTCGGACTCCCGCGGTA	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCCTGCCAATCCAGATTTGGC
46	TGCATTTTCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
47	CCGCTCAATTCACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
48	CTCGGAAAGGTGCAACTTTGGTGT	ACACCAAAGTTGCACCTTTCCGAG
49	AATTCGACCAGCAGAACGTCCCAT	ATGGGACGTTCTGCTGGTCGAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCGTGAGGTTGAGACTCTGGC
51	CCAACAACTGGAACGGGAACCCGC	GCGGGTTCCCGTTCCAGTTGTTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC
54	TCACATCCAAATATGGTCCGCGAA	TTCGCGGACCATATTTGGATGTGA
55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTCACACCGGCAGAC
56	CATCGCAGAGCATAAACACCCTCA	TGAGGGTGTTTATGCTCTGCGATG
57	GTTGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATACCAAC
58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
59	GGAATGAGTGGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
60	TGTCAATATGCGTCCGTGTCGTCT	AGACGACACGGACGCATATTGACA
61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCTGAGGCTCATCA
62	CACCGCGGTGTTCCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
64	TTAACCTGCGTCTGCCCCTTTCCT	AGGAAAGGGGCAGACGCAGGTTAA
65	AGGCGCGTTCCTGCCTTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
66	TAGGGCGATGGCACGAAGCTTCAA	TTGAAGCTTCGTGCCATCGCCCTA
67	TGCATAGAGCCAAAGTCGGCGATG	CATCGCCGACTTTGGCTCTATGCA
68	TTGAGAGGCAGGTGGCCACACGGA	TCCGTGTGGCCACCTGCCTCTCAA
69	TCCGCATTGTGAGAAAAAACGAGC	GCTCGTTTTTTCTCACAATGCGGA
70	GGCGGTTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAAACCGCC
71	GGTGAAAATTTCGTAGCCACGGGC	GCCCGTGGCTACGAAATTTTCACC
72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTCTTCATCCTCCGTCGG
73	CCAGTTTGGCCCAATTCGCCAAAA	TTTTGGCGAATTGGGCCAAACTGG
74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCCTAATAGATCC
75	CGGATGTCACCGTTTGGACTTTCA	TGAAAGTCCAAACGGTGACATCCG
76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTTGCGAT
77	CAGGGCATGCAATAATCGAGGTTC	GAACCTCGATTATTGCATGCCCTG
78	CATGCGTTGATATATGGGCCCAAG	CTTGGGCCCATATATCAACGCATG

79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
80	TTGTATGTCTGCCGACCGGCGACC	GGTCGCCGGTCGGCAGACATACAA
81	GATGGCGCCCGTTGATAGGTATGG	CCATACCTATCAACGGGCGCCATC
82	ATGAGAATCGCCGGCAATCTGCTA	TAGCAGATTGCCGGCGATTCTCAT
83	ATTTGCACTGACCGCAGGCTCGTG	CACGAGCCTGCGGTCAGTGCAAAT
84	CAGGGAGAACGGTTAAGTTCCCGT	ACGGGAACTTAACCGTTCTCCCTG
85	AGGCCGGCGATCGAGGAGTTTGGT	ACCAAACTCCTCGATCGCCGGCCT
86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
87	GTGCAACGCCGAGGACTTCCATCA	TGATGGAAGTCCTCGGCGTTGCAC
88	TCGGTGCCTGATAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
89	TGAAATACCACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTTCA
90	GCATCGTGTACATGACTGCCGCGA	TCGCGGCAGTCATGTACACGATGC
91	CAGTGTTCTAACGGCGCGCGTGAA	TTCACGCGCGCCGTTAGAACACTG
92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
93	CGAAAAACTAGTGGGCTCGCCGCG	CGCGGCGAGCCCACTAGTTTTTCG
94	CTTTCAGGGGAACTGCCGGAGTCG	CGACTCCGGCAGTTCCCCTGAAAG
95	TTGTGGCCTTCTTGTAAAGGCACG	CGTGCCTTTACAAGAAGGCCACAA
96	TCCACGAACGGCGACCCGTTGTCT	AGACAACGGGTCGCCGTTCGTGGA
97	CGACCTTGCACGAAACCTAACGAG	CTCGTTAGGTTTCGTGCAAGGTCG
98	GTGCAGCTTCACGAGCCAGCCTGA	TCAGGCTGGCTCGTGAAGCTGCAC
99	CGCTTTCGTGCGAATAGACGATGA	TCATCGTCTATTCGCACGAAAGCG
100	TGCGCTTACAGGCTCCTAGTGGTC	GACCACTAGGAGCCTGTAAGCGCA
101	CACGCGCTTAGTCGCGATCGCATA	TATGCGATCGCGACTAAGCGCGTG
102	CGGAGGGAGGGAGCTAGCCTTCGA	TCGAAGGCTAGCTCCCTCCCTCCG
103	GCATCCGGCCTGTTGATGACGCCT	AGGCGTCATCAACAGGCCGGATGC
104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
105	CCTTCCAATGATTGCATACGCCCA	TGGGCGTATGCAATCATTGGAAGG
106	AACACTTGATCAGGCGGGTCGTCT	AGACGACCCGCCTGATCAAGTGTT
107	TGGAATCAAGGCCGTAAAGGACAG	CTGTCCTTTACGGCCTTGATTCCA
108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
109	AGTGGTGAATGGCCGCTACCCTGA	TCAGGGTAGCGGCCATTCACCACT
110	TGTTGAAGCGAGCTAAAACGGCCA	TGGCCGTTTTAGCTCGCTTCAACA
111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
112	AAGGTGGTGCCATTCATTTGGCTA	TAGCCAAATGAATGGCACCACCTT
113	CGTTAAACCGCAATCCGTTCGGCT	AGCCGAACGGATTGCGGTTTAACG
114	CACGAGATACCGGCGTAAGGGTGG	CCACCCTTACGCCGGTATCTCGTG
115	CTACGGCAAACGTGTGGAATGGGT	ACCCATTCCACACGTTTGCCGTAG
116	GTAGGGCGATGACGGGCGAACTAC	GTAGTTCGCCCGTCATCGCCCTAC
117	AATCGACCTCCGCACACATTCGCA	TGCGAATGTGTGCGGAGGTCGATT
118	GAGTCAGCATGGCGGCGGAGATTC	GAATCTCCGCCGCCATGCTGACTC
119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTTGCCAGCGTCTTTATCT

120	GGTACCTCAACGCGAACCACTTGT	ACAAGTGGTTCGCGTTGAGGTACC
121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTTGGGTAGCCATCGCTT
122	AGAGCTTATGCAGAACCAGGCGCC	GGCGCCTGGTTCTGCATAAGCTCT
123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCCTGCGTGAGACCGAT
124	TAGGTTGCCCGCCAGAAGAAACAT	ATGTTTCTTCTGGCGGGCAACCTA
125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTTGCAACAGCACCG
126	TGATGAAAGTTTGCGGCAGGACAC	GTGTCCTGCCGCAAACTTTCATCA
127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
128	AACATTGCGCGGTCCACCAGGGTT	AACCCTGGTGGACCGCGCAATGTT
129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCCC
130	TCGAGCTGGTCCCCGTGAACGTGT	ACACGTTCACGGGGACCAGCTCGA
131	GTCTTGGGGGCCGCTTAGTGAAAA	TTTTCACTAAGCGGCCCCCAAGAC
132	ACTGTTGGCTTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
133	AGGACCATTCGGAAGGCGAAGATA	TATCTTCGCCTTCCGAATGGTCCT
134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCTCCCAAG
135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCCGTTTATT
136	TTGTACGTGCGGTCCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
137	CGCACCAAACTGAGTTTCCCAGAC	GTCTGGGAAACTCAGTTTGGTGCG
138	ACCTGATCGTTCCCCTATTGGGAA	TTCCCAATAGGGGAACGATCAGGT
139	GGAACAGAGGCGAGGGGACTGAGC	GCTCAGTCCCCTCGCCTCTGTTCC
140	CCCTGCCTTGGCGTGTCGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
141	ACTCTGACACGCCAACTCCGGAAG	CTTCCGGAGTTGGCGTGTCAGAGT
142	CTGACGGTTTTCATTCGGCGTGCC	GGCACGCCGAATGAAAACCGTCAG
143	TGCGGTGGTTCATTGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGGCCATGC
145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTCGCTTTACGGCCT
146	CGAATATTATGCCGAGAATCCGCG	CGCGGATTCTCGGCATAATATTCG
147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
148	GGACGGTTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAAACCGTCC
149	AAAGGCTATTGAGTTGGTTGGGCG	CGCCCAACCAACTCAATAGCCTTT
150	GATGGCCTATTCGGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
151	GATCCAGTAGGCAGCTTCATCCCA	TGGGATGAAGCTGCCTACTGGATC
152	AATAACTCGCGCGGGTATGCTTCT	AGAAGCATACCCGCGCGAGTTATT
153	GGAGGAGGTTTGTCTCGGAAAGCA	TGCTTTCCGAGACAAACCTCCTCC
154	CTTTGGTATGGCACATGCTGCCCG	CGGGCAGCATGTGCCATACCAAAG
155	AGAAAGGCTCGAGCAACGGGAACT	AGTTCCCGTTGCTCGAGCCTTTCT
156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCGGACCAGTGCGGTAGATT
157	CGTGGCGGCCACAGTTTTTGGAGG	CCTCCAAAAACTGTGGCCGCCACG
158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGGATTGAACTGCAA
159	GGCCCAAAGCCCCAGACCATTTTA	TAAAATGGTCTGGGGCTTTGGGCC
160	CGCCTGTCTTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG

161	TGAGGCAACAGGGGCCAAAAACTA	TAGTTTTTGGCCCCTGTTGCCTCA
162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAAGCCTTGGGGCC
164	GCACGTGAAGTTTAACCGCGATTC	GAATCGCGGTTAAACTTCACGTGC
165	AGCGGCAGAAACGTTCCTTGACGG	CCGTCAAGGAACGTTTCTGCCGCT
166	TCGTCGAGCAGACGAGATTGCACG	CGTGCAATCTCGTCTGCTCGACGA
167	TCTTTGCCGCGTAACTGACTGCTT	AAGCAGTCAGTTACGCGGCAAAGA
168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTTGGCACATAAA
169	TGTTACTGTGGTTCACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
170	CGCGCCTCGCTAGACCTTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
171	ACAAATGCGTGAGAGCTCCCAACT	AGTTGGGAGCTCTCACGCATTTGT
172	CGCGCAGATTATAGACCCGAATGT	ACATTCGGGTCTATAATCTGCGCG
173	CAAATAACGCCGCTGAATCGGCGT	ACGCCGATTCAGCGGCGTTATTTG
174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTTGCTCGTGTTCA
176	CAGCAGATCCTTCGTAGCGGTCGT	ACGACCGCTACGAAGGATCTGCTG
177	GGAACCTGGTGAGTTGTGCCTCAT	ATGAGGCACAACTCACCAGGTTCC
178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTCGCTTATGA
179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
180	TGTCAGAGCCCGCGACTCAGACGG	CCGTCTGAGTCGCGGGCTCTGACA
181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
182	CTCAGAAGTCCTCGGCGAACTGGG	CCCAGTTCGCCGAGGACTTCTGAG
183	ATCCTTTTATCTACTCCGCGGCGA	TCGCCGCGGAGTAGATAAAAGGAT
184	AGGCGTGCAGCAACAGGATAAACC	GGTTTATCCTGTTGCTGCACGCCT
185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
187	TCCACTATAACTGCGGGTCCGTGT	ACACGGACCCGCAGTTATAGTGGA
188	GCCCAGTCGGCTCTAACAAGTTCG	CGAACTTGTTAGAGCCGACTGGGC
189	CGGAACGGATAATCGGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
190	TAAAATAAGCGCCTGGCGGGAGGA	TCCTCCCGCCAGGCGCTTATTTTA
191	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC
192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAACT
193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
194	TTCGCAGCACCCGCTAGGTACAGT	ACTGTACCTAGCGGGTGCTGCGAA
195	TAACCCGATTTTTGCGACTCTGCC	GGCAGAGTCGCAAAAATCGGGTTA
196	CGTCGCATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCAATGCGACG
197	GAGCTGACGTCACCATCAGAGGAA	TTCCTCTGATGGTGACGTCAGCTC
198	GGAGGCTGGGGGTCGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
199	TTGTGGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCCACAA
200	CCCTCGCACTGTGTTCACCCTCTT	AAGAGGGTGAACACAGTGCGAGGG
201	TCATTGACTCGAATCCGCACAACG	CGTTGTGCGGATTCGAGTCAATGA

202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTCGTTTCATGTCCGCGC
206	CTTATTGGGTGCCGGTGTCGGATT	AATCCGACACCGGCACCCAATAAG
207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTTTGGTAACCGCCCC
208	GCTAAAGCGTGCTCCGTAACTGCC	GGCAGTTACGGAGCACGCTTTAGC
209	ATCTCATGCATCTCGGTTCGTCGT	ACGACGAACCGAGATGCATGAGAT
210	ACGAAAAAAGTGTGCGGATCCCCT	AGGGGATCCGCACACTTTTTTCGT
211	CCAAGTACACCGCACGCATGTTTA	TAAACATGCGTGCGGTGTACTTGG
212	ATCGTGCGTGGAGTGTCGCATCTA	TAGATGCGACACTCCACGCACGAT
213	TCCAGATACCGCCCCGAACTTTGA	TCAAAGTTCGGGGCGGTATCTGGA
214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
215	TTGAAATTGCTCTGCCGTCAGTCA	TGACTGACGGCAGAGCAATTTCAA
216	AGTCAGGCGAGATGTTCAGGCAGC	GCTGCCTGAACATCTCGCCTGACT
217	ACAAGCCGACGTTAAGCCCGCCCA	TGGGCGGGCTTAACGTCGGCTTGT
218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
219	GTGAGACACACATCCCCTCCAATG	CATTGGAGGGGATGTGTGTCTCAC
220	CGACGGATGCAGAGTTCAGTGGTC	GACCACTGAACTCTGCATCCGTCG
221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
222	TTAGCAAAGCGGCGCCGTTAGCAA	TTGCTAACGGCGCCGCTTTGCTAA
223	CCCGACACGGGTCAGCGTAATAAT	ATTATTACGCTGACCCGTGTCGGG
224	GCGACGGCCCTGAGGTATGTCGTC	GACGACATACCTCAGGGCCGTCGC
225	CAAAAGTGTGTTCCCTTGCGCTTG	CAAGCGCAAGGGAACACACTTTTG
226	TCTCGAAGCACAGCCCGGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
227	ATGCTAACCGTTGGCCATGGAACT	AGTTCCATGGCCAACGGTTAGCAT
228	CTTGCGGAGTGTTAGCCCAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA
230	CCAATGCCTTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
231	AGCAGATAACGTCCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
232	TTGACCATTACGTGTTGCGCCCAT	ATGGGCGCAACACGTAATGGTCAA
233	TCGCGTATTTGCGGAATTCGTCTG	CAGACGAATTCCGCAAATACGCGA
234	CTGCGTGTCAACAATGTCCCGCAG	CTGCGGGACATTGTTGACACGCAG
235	TCTGGTGCCACGCAAGGTCCACAG	CTGTGGACCTTGCGTGGCACCAGA
236	CTCCGGGAGGTCACTTAATTGCGG	CCGCAATTAAGTGACCTCCCGGAG
237	TTTTCGTGATTGCCCGGAGGAGGC	GCCTCCTCCGGGCAATCACGAAAA
238	TCGGGATGTAGCTGGGGCTACCGG	CCGGTAGCCCCAGCTACATCCCGA
239	CGAGCCAACGCAAACACGTCCTTG	CAAGGACGTGTTTGCGTTGGCTCG
240	GCAAAGCCTTTGTGGGGCGGTAGT	ACTACCGCCCCACAAAGGCTTTGC
241	ATTCGACCGGAAATGAGGTCTTCG	CGAAGACCTCATTTCCGGTCGAAT
242	TTCGCTTGCTGAGTTGCTCTGTTC	GAACAGAGCAACTCAGCAAGCGAA

243	CGCGTGAAGACCCCATTCCCGAGT	ACTCGGGAATGGGGTCTTCACGCG
244	AACCGTATTCGCGGTCACTTGTGG	CCACAAGTGACCGCGAATACGGTT
245	GGGGCCAACCGTTTCGAGGCGTAT	ATACGCCTCGAAACGGTTGGCCCC
246	TTCGGCTGGCAGTCCAAACGGCTT	AAGCCGTTTGGACTGCCAGCCGAA
247	GGGTGTGGTTAGAATGCACGGTTC	GAACCGTGCATTCTAACCACACCC
248	GCGAGGACCGAACTAGACAAACGG	CCGTTTGTCTAGTTCGGTCCTCGC
249	ACGCACGCGTGACCGAAGTTGCTG	CAGCAACTTCGGTCACGCGTGCGT
250	TAAAAGGTCGCTTTGAAAGGGGGA	TCCCCCTTTCAAAGCGACCTTTTA
251	TGCGATCGCTAACTGCTGGGACAA	TTGTCCCAGCAGTTAGCGATCGCA
252	GGAGGTATAAGCGGAGCGGCCTCA	TGAGGCCGCTCCGCTTATACCTCC
253	ATGCTGACATGTCGTGCACCTCGT	ACGAGGTGCACGACATGTCAGCAT
254	TGTGGTTAAAGCGTCCGTTCAACG	CGTTGAACGGACGCTTTAACCACA
255	CGTTCACACCGGCGTAAGCTGCGT	ACGCAGCTTACGCCGGTGTGAACG
256	CCTATCCCGGCGAGAACTTCTGTG	CACAGAAGTTCTCGCCGGGATAGG
257	GTCTGCACTCACGCAGCGGAGGGA	TCCCTCCGCTGCGTGAGTGCAGAC
258	GCACGAGTTGGTGCTCGGCAGATT	AATCTGCCGAGCACCAACTCGTGC
259	AACGTCGCACGACACACGTTCGTC	GACGAACGTGTGTCGTGCGACGTT
260	ATGCGCGCTTATCCTAGCATGGTC	GACCATGCTAGGATAAGCGCGCAT
261	TCACGTTTTCGTCTCGACATGAGG	CCTCATGTCGAGACGAAAACGTGA
262	TGTGCCTCATCCTTAGGATACGGC	GCCGTATCCTAAGGATGAGGCACA
263	AGGTGGTGTGGGTCAACCGCTTTA	TAAAGCGGTTGACCCACACCACCT
264	CTGGATCGAAGGGACTGCAAGCTC	GAGCTTGCAGTCCCTTCGATCCAG
265	TAGATCAACTCGCGTACGCATGGA	TCCATGCGTACGCGAGTTGATCTA
266	GATCCTGCGGAGAAGAGAGTGCAG	CTGCACTCTCTTCTCCGCAGGATC
267	TACGTGTGGAGATGCCCCGAACCG	CGGTTCGGGGCATCTCCACACGTA
268	GCGCTATGTCAATCGTGGGCGTAG	CTACGCCCACGATTGACATAGCGC
269	AGCGAGGTTTCTAGCGTCGACACC	GGTGTCGACGCTAGAAACCTCGCT
270	ACCCAGGTTTTGCCGTTGTGGAAT	ATTCCACAACGGCAAAACCTGGGT
271	CCCTGTTAACGGCTGCGTAGTCTC	GAGACTACGCAGCCGTTAACAGGG
272	AGGCCGATTTCACCCGCCAATTGC	GCAATTGGCGGGTGAAATCGGCCT
273	GAGCCCTCACTCCTTGCCCTTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
274	GGGTGGACATCCGCCTCGCAGTCA	TGACTGCGAGGCGGATGTCCACCC
275	GATGGCTGAGAACCGTGCTACGAT	ATCGTAGCACGGTTCTCAGCCATC
276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCCTAACGTCGA
277	CGAATGGGTCTGGACCTTGCATAG	CTATGCAAGGTCCAGACCCATTCG
278	GTGCACCAGACATTCGAACTCGGA	TCCGAGTTCGAATGTCTGGTGCAC
279	AGAGGCCCCGTATATCCCATCCAT	ATGGATGGGATATACGGGGCCTCT
280	AACGCCTGTTCAGAGCATCAGCGG	CCGCTGATGCTCTGAACAGGCGTT
281	AAGGCTCAACACGCCTATGTGCGC	GCGCACATAGGCGTGTTGAGCCTT
282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
283	ATGTCCCATGTAAAGACGCGTGTG	CACACGCGTCTTTACATGGGACAT

284	ATGGAGTCTGCTCACGCCCAAAGG	CCTTTGGGCGTGAGCAGACTCCAT
285	CGGCCTCCAACAAGGAGCACTAAC	GTTAGTGCTCCTTGTTGGAGGCCG
286	CAGAGCCGTGGCAACATTGCGAGC	GCTCGCAATGTTGCCACGGCTCTG
287	TCATTTGAATGAGGTGCGCACCGG	CCGGTGCGCACCTCATTCAAATGA
288	GACGTACCGGAAGCGCCGTATAAA	TTTATACGGCGCTTCCGGTACGTC
289	ATGCGAGCAATGGGATCCGGATTC	GAATCCGGATCCCATTGCTCGCAT
290	AGAGTGAGGCCTCCCTGACCAGTG	CACTGGTCAGGGAGGCCTCACTCT
291	CGCACCGTAAGTAGATTTGCCCGC	GCGGGCAAATCTACTTACGGTGCG
292	TGAACCTTTGAGCACGTCGTGCGC	GCGCACGACGTGCTCAAAGGTTCA
293	TCCGCCTTTTTGGTTACCTCGAAG	CTTCGAGGTAACCAAAAAGGCGGA
294	GAACGCCAACGGCACTAACACATC	GATGTGTTAGTGCCGTTGGCGTTC
295	CCGACAGCAGCCAAGACGTCCCAG	CTGGGACGTCTTGGCTGCTGTCGG
296	CATAAAAAAACCTGGGGCTCTGCG	CGCAGAGCCCCAGGTTTTTTTATG
297	TGCCAACTGTGCAGACCGGACTTA	TAAGTCCGGTCTGCACAGTTGGCA
298	GGCGAAAGAGCGAAACCGGCTCGT	ACGAGCCGGTTTCGCTCTTTCGCC
299	GGGATGCGTATTTTAGCGAACACG	CGTGTTCGCTAAAATACGCATCCC
300	TGGGATTCAGCGACCAGTACGCGA	TCGCGTACTGGTCGCTGAATCCCA
301	CCCGATATTCGCCCGGCCTATTCG	CGAATAGGCCGGGCGAATATCGGG
302	CGAGAAGATGCCTCACGCAACCAA	TTGGTTGCGTGAGGCATCTTCTCG
303	AACCTTGACCCGTGGATGACGCTA	TAGCGTCATCCACGGGTCAAGGTT
304	GGCTAGACGATGGATACCCGTGCC	GGCACGGGTATCCATCGTCTAGCC
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306	GCTTCCGGATGAACGGGATGGTTG	CAACCATCCCGTTCATCCGGAAGC
307	CCCTCCATGTTCTTCGAACGGTTT	AAACCGTTCGAAGAACATGGAGGG
308	TTGATGGGCGGCAATGCTCTTGCT	AGCAAGAGCATTGCCGCCCATCAA
309	ATTGTGAGATGCGCCAAATTCCCC	GGGGAATTTGGCGCATCTCACAAT
310	TCAGCACAGCCAGACGGTCAACTT	AAGTTGACCGTCTGGCTGTGCTGA
311	ACTCCACTCCTCGGTGGCAAACTA	TAGTTTGCCACCGAGGAGTGGAGT
312	TCTGGGCATGCCTGGACGGAGACG	CGTCTCCGTCCAGGCATGCCCAGA
313	TCTCAACTCCGGTACGACGAAACA	TGTTTCGTCGTACCGGAGTTGAGA
314	TTGCGTGGTCAAAGGCGCAACGTG	CACGTTGCGCCTTTGACCACGCAA
315	AGACAGCGATCCGCGGCTCATGAT	ATCATGAGCCGCGGATCGCTGTCT
316	CGCGTCTCTAACTGAGAGCAGCCA	TGGCTGCTCTCAGTTAGAGACGCG
317	AGGCGCACATGTACGGACATTCAG	CTGAATGTCCGTACATGTGCGCCT
318	GATGAGTGGCACGTCGGTGTGTAA	TTACACACCGACGTGCCACTCATC
319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCCGGCAGGT
321	AGCATTGGCGTTTTTCCGCAACGA	TCGTTGCGGAAAAACGCCAATGCT
322	GGTAATATTCAGCGCGACCGCTCA	TGAGCGGTCGCGCTGAATATTACC
323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTCGTACGCTAT
324	TAGGTCACGATGCGTTTGACGCTA	TAGCGTCAAACGCATCGTGACCTA

325	ACTGCCCGTACCTCTGGTTCTGGC	GCCAGAACCAGAGGTACGGGCAGT
326	CCTTTGGCCTGAAGTTGTCGTAGC	GCTACGACAACTTCAGGCCAAAGG
327	GTGCCCCACGAGCGTATCGTTGTA	TACAACGATACGCTCGTGGGGCAC
328	AGGCGCTACGTGGGCCTGGAGCAA	TTGCTCCAGGCCCACGTAGCGCCT
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330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCGCGTGGT
331	CCATGATGCATTGGGTGCATTTAG	CTAAATGCACCCAATGCATCATGG
332	GGTCCGGCCCTACGAAACGTTCGA	TCGAACGTTTCGTAGGGCCGGACC
333	CCGTGTGGCTGGAGATTCGTGTGA	TCACACGAATCTCCAGCCACACGG
334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
335	GGGTCAGTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
336	GCCGTGAAGTCGAATGCAGATCGA	TCGATCTGCATTCGACTTCACGGC
337	GCCACCACCCAGTGCATTCAGGTA	TACCTGAATGCACTGGGTGGTGGC
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339	TGTTTGCCGCCATTAGGGAGTAAC	GTTACTCCCTAATGGCGGCAAACA
340	GCTCCGCTGGATGTGCCGGTTTAG	CTAAACCGGCACATCCAGCGGAGC
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344	TTGCGACTCGACTTGGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
345	TCTGGGAGCTGTTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCCAGA
346	TGCACGCGGAACTCCCTTTACCAT	ATGGTAAAGGGAGTTCCGCGTGCA
347	TGGCAGCAAATGAATCGAAAGCAC	GTGCTTTCGATTCATTTGCTGCCA
348	AACTGGTGACGCGGTACAGCGAAG	CTTCGCTGTACCGCGTCACCAGTT
349	AGACGATTACGCTGGACGCCGTCG	CGACGGCGTCCAGCGTAATCGTCT
350	ATGCCCTCCTTCATGGAAAGGGTT	AACCCTTTCCATGAAGGAGGGCAT
351	ATTCTCGGAGCGTATGCGCCAGAA	TTCTGGCGCATACGCTCCGAGAAT
352	ATAGCGGAGTTTGGGTACGCGAAC	GTTCGCGTACCCAAACTCCGCTAT
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355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTGATGCTAACAGG
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357	TGAGAGAGGCGTTGGTTAAGGCAA	TTGCCTTAACCAACGCCTCTCTCA
358	AAGCAGGCGAAGGGATACTCCTCG	CGAGGAGTATCCCTTCGCCTGCTT
359	TCACGACAGACGGGCCGAGATTAC	GTAATCTCGGCCCGTCTGTCGTGA
360	AAGCAATTTGGCCTCGTTTTGTGA	TCACAAAACGAGGCCAAATTGCTT
361	GCTGGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
362	TTGTGAATCCGTTCTGTCCCCGAC	GTCGGGGACAGAACGGATTCACAA
363	TGGGCTCCTCTGAGGCGAGATGGC	GCCATCTCGCCTCAGAGGAGCCCA
364	GGATAGAGTGAATCGACCGGCAAC	GTTGCCGGTCGATTCACTCTATCC
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366	GCCAGTATTCTCGGGTGTTGGACG	CGTCCAACACCCGAGAATACTGGC
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368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
369	CGCGTCCCAGCGCCCTTGGAGTAT	ATACTCCAAGGGCGCTGGGACGCG
370	ATGAAGCCTACCGGGCGACTTCGT	ACGAAGTCGCCCGGTAGGCTTCAT
371	CCAGACAGATGGCCTGGAACCATG	CATGGTTCCAGGCCATCTGTCTGG
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373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCATGCGG
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376	TGCGAGGTGAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
377	GGGCCGCATTCTTGATGTCCATTC	GAATGGACATCAAGAATGCGGCCC
378	CCTCGGATGTGGGCTCTCGCCTAG	CTAGGCGAGAGCCCACATCCGAGG
379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTCACGCCAACATGCCTA
380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTTCGTATCG
381	TACGCCGGTTAGCACGGTGCGCTA	TAGCGCACCGTGCTAACCGGCGTA
382	CATACGATGTCCGGGCCGTGTCGC	GCGACACGGCCCGGACATCGTATG
383	ATCCGCAGTTGTATGGCGCGTTAT	ATAACGCGCCATACAACTGCGGAT
384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCATCTTTGTCCCTTACCC
385	ATTGGAGTGTTTTGGTGAATCCGC	GCGGATTCACCAAAACACTCCAAT
386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTTC
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388	ACCTGCTTTTGGGTGGGTGATATG	CATATCACCCACCCAAAAGCAGGT
389	AATCGTGGGCGCAGCAAACGTATA	TATACGTTTGCTGCGCCCACGATT
390	GTCGCCGGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGCGAC
391	ACCCGTCGATGCTTCCTCCTCAGA	TCTGAGGAGGAAGCATCGACGGGT
392	ATCCGGGTGGGCGATACAAGAGAT	ATCTCTTGTATCGCCCACCCGGAT
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394	GCAAAGTCCCACTGGCAAGCCGAT	ATCGGCTTGCCAGTGGGACTTTGC
395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTCG
396	CTCATGAGCGCAGTTGTGCGTGAG	CTCACGCACAACTGCGCTCATGAG
397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTTCATCTG
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409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
410	GCCCGCTAATCCGACACCCAGTTT	AAACTGGGTGTCGGATTAGCGGGC
411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
412	GAATCACCGAATCACCGACTCGTT	AACGAGTCGGTGATTCGGTGATTC
413	AACCAGCCGCAGTAGCTTACGTCG	CGACGTAAGCTACTGCGGCTGGTT
414	TTTTCTGAGGGACACGCGGGCGTT	AACGCCCGCGTGTCCCTCAGAAAA
415	GGTGCTCCGTTTGATCGATCCTCC	GGAGGATCGATCAAACGGAGCACC
416	CCGCTTAGGCCATACTCTGAGCCA	TGGCTCAGAGTATGGCCTAAGCGG
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423	AGCGGGATCCCAGAGTTTCGAAAA	TTTTCGAAACTCTGGGATCCCGCT
424	GAGCTTGAGAGCGAGGTCATCCTC	GAGGATGACCTCGCTCTCAAGCTC
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431	TCGTGTAGACTCGGCGACAGGCGT	ACGCCTGTCGCCGAGTCTACACGA
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435	TCCTACATGTCGCGTCACGATCAC	GTGATCGTGACGCGACATGTAGGA
436	GACCGATCGCGAAGTCGTACACAT	ATGTGTACGACTTCGCGATCGGTC
437	GTCGCCAGGACTGGGCCGATGTGA	TCACATCGGCCCAGTCCTGGCGAC
438	ACCGATAAGACTTGCATCCGAACG	CGTTCGGATGCAAGTCTTATCGGT
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445	AGGCATCGTGCCGGATTGCTCCCT	AGGGAGCAATCCGGCACGATGCCT
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447	TTCGGGTCACATCCGATGCCATAC	GTATGGCATCGGATGTGACCCGAA

448	ACCCATCGCCGGAAAGCGATGTTG	CAACATCGCTTTCCGGCGATGGGT
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450	ACTTCCAAGTCCTTGACCGTCCGA	TCGGACGGTCAAGGACTTGGAAGT
451	TCTCAATATTCCCGTAGTCGCCCA	TGGGCGACTACGGGAATATTGAGA
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453	CGTCCTCCATGTTGTCACGAACAG	CTGTTCGTGACAACATGGAGGACG
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459	AGGGTACGTGTCGCAGCTTCGCGT	ACGCGAAGCTGCGACACGTACCCT
460	ACCCTTGCTCCGCCATGTCTCTCA	TGAGAGACATGGCGGAGCAAGGGT
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462	TGTCGTTGCTCCCGAGTACCATTG	CAATGGTACTCGGGAGCAACGACA
463	GTTGTCCGAGACGTTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC
464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTCGTGAGTGTTCACCAGC
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466	CCCATCACAACGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
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471	GCGGCTATGTGATGACGGCCTAGC	GCTAGGCCGTCATCACATAGCCGC
472	AGTACACGGGCGTGTTAGCGCTCC	GGAGCGCTAACACGCCCGTGTACT
473	TCCTGTGTGGTGGCGCACTCCCAC	GTGGGAGTGCGCCACCACACAGGA
474	CCAACTAACCAATCGCGCGGATGA	TCATCCGCGCGATTGGTTAGTTGG
475	AGTGAGTGACCAAGGCAGGAGCAA	TTGCTCCTGCCTTGGTCACTCACT
476	CATCTTTCGCGGAGTTTATTGCGG	CCGCAATAAACTCCGCGAAAGATG
477	CTTCGTCCGGTTAGTGCGACAGCA	TGCTGTCGCACTAACCGGACGAAG
478	CTCACGAAAACGTGGGCCCGAAAT	ATTTCGGGCCCACGTTTTCGTGAG
479	CGCAGCAGCTGAACTCTAGCATTG	CAATGCTAGAGTTCAGCTGCTGCG
480	AGGAGACATACGCCCAAATGGTGC	GCACCATTTGGGCGTATGTCTCCT
481	ATTGAGAACTCGTGCGGGAGTTTG	CAAACTCCCGCACGAGTTCTCAAT
482	CTCTTTGTAGGCCCAGGAGGAGCA	TGCTCCTCCTGGGCCTACAAAGAG
483	GCCGCAGGGTCGATAATTGGTCTA	TAGACCAATTATCGACCCTGCGGC
484	AAACGCCGCCCTGAGACTATTGGG	CCCAATAGTCTCAGGGCGGCGTTT
485	CTGAGTTGCCTGGAACGTTGGACT	AGTCCAACGTTCCAGGCAACTCAG
486	CGGATGGGTTGCAGAGTATGGGAT	ATCCCATACTCTGCAACCCATCCG
487	CTGACCTTTGGGGGTTAGTGCGGT	ACCGCACTAACCCCCAAAGGTCAG
488	GGAAATGAGAACCTTACCCCAGCG	CGCTGGGGTAAGGTTCTCATTTCC

489	AACGCATCGTCCGTCAACTCATCA	TGATGAGTTGACGGACGATGCGTT
490	TGGAGAGAGACTTCGGCCATTGTT	AACAATGGCCGAAGTCTCTCTCCA
491	TTGCGCTCATTGGATCTTGTCAGG	CCTGACAAGATCCAATGAGCGCAA
492	AGCGCGTTAAAGCACGGCAACATT	AATGTTGCCGTGCTTTAACGCGCT
493	AGCCAGTAAACTGTGGGCGGCTGT	ACAGCCGCCCACAGTTTACTGGCT
494	CGACTGATGTGCAACCAGCAGCTG	CAGCTGCTGGTTGCACATCAGTCG
495	GGTTGCTCATACGACGAGCGAGTG	CACTCGCTCGTCGTATGAGCAACC
496	GCGCAAATCCACGGAACCCGTACC	GGTACGGGTTCCGTGGATTTGCGC
497	ACGCAGTTTATTCCCCTGGCTTCT	AGAAGCCAGGGGAATAAACTGCGT
498	AGAACCTCCGCGCCTCCGTAGTAG	CTACTACGGAGGCGCGGAGGTTCT
499	AAAGGAGCTTTCGCCCAACGTACC	GGTACGTTGGGCGAAAGCTCCTTT
500	AGTGATTGTGCCACTCCACAGCTC	GAGCTGTGGAGTGGCACAATCACT
501	GCGATCGTCGAGGGTTGAGCTGAA	TTCAGCTCAACCCTCGACGATCGC
502	GGGAGACAGCCATTATGGTCCTCG	CGAGGACCATAATGGCTGTCTCCC
503	GAGACGCTGTCACTCCGGCAGAAC	GTTCTGCCGGAGTGACAGCGTCTC
504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG
505	CGGCATAACGTCCAGTCCTGGGAC	GTCCCAGGACTGGACGTTATGCCG
506	AAGCGGAACGGGTTATACCGAGGT	ACCTCGGTATAACCCGTTCCGCTT
507	TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
508	AGGGAACCGCGTTCAAACTCAGTT	AACTGAGTTTGAACGCGGTTCCCT
509	GAATTACAACCACCCGCTCGTGTT	AACACGAGCGGGTGGTTGTAATTC
510	TTCAGTGCTCACGAAGCATGGATT	AATCCATGCTTCGTGAGCACTGAA
511	TTAGTTTGGCGTTGGGACTTCACC	GGTGAAGTCCCAACGCCAAACTAA
512	AATGCGACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
513	CCGAAACCGTTAACGTGGCGCACA	TGTGCGCCACGTTAACGGTTTCGG
514	TAAAGTAACAAGGCGACCTCCCGC	GCGGGAGGTCGCCTTGTTACTTTA
515	TAATGATTTTAGTCGCGGGGTGGG	CCCACCCCGCGACTAAAATCATTA
516	GGCTACTCTAAGTGCCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCCGCCA
518	GGGCGTTAGGCGTAATAGACCGTC	GACGGTCTATTACGCCTAACGCCC
519	GCCACCTTTAGACGGCGGCTCTAG	CTAGAGCCGCCGTCTAAAGGTGGC
520	GAGATGTGTAAACGTGCAGGCACC	GGTGCCTGCACGTTTACACATCTC
521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGGAGGGCCACGAGCTA
522	GTGTCGGCGCTATTTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
523	CCAGGGAAGCAACTGGTTGCCATT	AATGGCAACCAGTTGCTTCCCTGG
524	TTCCGAAACTAAGCCAGAACCGCT	AGCGGTTCTGGCTTAGTTTCGGAA
525	GCAAACCCGGTAACCCGAGAGTTC	GAACTCTCGGGTTACCGGGTTTGC
526	GCAAATGGCGTCATGCACGAACGT	ACGTTCGTGCATGACGCCATTTGC
527	AGTACTTTCGCGCCCAGTTTAGGG	CCCTAAACTGGGCGCGAAAGTACT
528	AAGATCTGCGAGGCATCCCGGCTT	AAGCCGGGATGCCTCGCAGATCTT
529	GCAAGTGTATCGCACAGTGCGATT	AATCGCACTGTGCGATACACTTGC

530	CCGACAAGGCCTCAATTCATTCTG	CAGAATGAATTGAGGCCTTGTCGG
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533	GTCACCAGGAGGGAAGTTTCACCC	GGGTGAAACTTCCCTCCTGGTGAC
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538	TTGGCCAGGAATATGGTCTCGAGA	TCTCGAGACCATATTCCTGGCCAA
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543	ATACCTCCGCAGAACCATTCCGTT	AACGGAATGGTTCTGCGGAGGTAT
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545	TGCTCAATTTGTGCAGAAAACGCC	GGCGTTTTCTGCACAAATTGAGCA
546	TTATCGCGAGAGACGACCGTGTCC	GGACACGGTCGTCTCTCGCGATAA
547	GACGCGACGTGAGTAGTGGAAGCG	CGCTTCCACTACTCACGTCGCGTC
548	ATGGTAGGGGCATTGGGCTTTCCT	AGGAAAGCCCAATGCCCCTACCAT
549	CCAAATATAGCCGCGCGGAGACAT	ATGTCTCCGCGCGGCTATATTTGG
550	GCAAACCCTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTTGC
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554	CATATCAGCGTCGTCTAGCTCGCG	CGCGAGCTAGACGACGCTGATATG
555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
556	GGCCCCGACACTACAGGGTAATCA	TGATTACCCTGTAGTGTCGGGGCC
557	GGCTCCAGGGCGAGATTATGAATG	CATTCATAATCTCGCCCTGGAGCC
558	CAAAATCCGATGGGCGGAAAATTA	TAATTTTCCGCCCATCGGATTTTG
559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
560	TAGCTATTGCCCCGATGGGCTACT	AGTAGCCCATCGGGGCAATAGCTA
561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
562	GACGCTGTGGCTCGGAAACTGTTC	GAACAGTTTCCGAGCCACAGCGTC
563	CCTGGGTTCGCCGCGTGGTAACTG	CAGTTACCACGCGGCGAACCCAGG
564	TTCCCGCGTAGCCCAACAGCTATA	TATAGCTGTTGGGCTACGCGGGAA
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566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTTCGGTGCCATTTTT
567	CATTCCGCGCGAGTTGAAATCCAG	CTGGATTTCAACTCGCGCGGAATG
568	ACGCACGTTTTTTGGCACGGTTAA	TTAACCGTGCCAAAAAACGTGCGT
569	TGTCCATGACGTCGTTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
570	TCTCAGTCGGACTCGTATGCCAGA	TCTGGCATACGAGTCCGACTGAGA

571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGTGCGTTTGGAG
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573	GGTGTCGGAGGGTGGTGACCTCGA	TCGAGGTCACCACCCTCCGACACC
574	AGCGCTTTTGGTCATGATTTGCAA	TTGCAAATCATGACCAAAAGCGCT
575	CCGAGGACTTACGTCTGCCCAGGA	TCCTGGGCAGACGTAAGTCCTCGG
576	GCCCAATCCAGTTCTTATGCGCCC	GGGCGCATAAGAACTGGATTGGGC
577	CGGGTTAACCCACGCAAGTTATGA	TCATAACTTGCGTGGGTTAACCCG
578	TGATTAGCGCTCAATACACGCGTG	CACGCGTGTATTGAGCGCTAATCA
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581	GCCATGTTCAAGGGCCTTTCGAAG	CTTCGAAAGGCCCTTGAACATGGC
582	CGCGGTGTTTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
584	CGATACGCGCCGGTTTGTTAAATC	GATTTAACAAACCGGCGCGTATCG
585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTTATAGCC
586	TGGGTAAATCACTATTGCGCGGTT	AACCGCGCAATAGTGATTTACCCA
587	GTCTTCATCGGCCCGCGCAAGCTA	TAGCTTGCGCGGGCCGATGAAGAC
588	GCGACACACCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCGC
589	GTAGCAGGGTCCGCAAGACCAAGC	GCTTGGTCTTGCGGACCCTGCTAC
590	TCGCCAACGCAGGGTAACTGCCAT	ATGGCAGTTACCCTGCGTTGGCGA
591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTCGGAGT
592	TCCCGCCCACTAGACTGACTCGTA	TACGAGTCAGTCTAGTGGGCGGGA
593	ACCTTCTGGGGTCGCTCACCAATA	TATTGGTGAGCGACCCCAGAAGGT
594	ATCATCCCACGGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGGATGAT
595	CGCTGGACTGGCCTATCCGAGTCG	CGACTCGGATAGGCCAGTCCAGCG
596	CGGTCTCAGCAACACTGTCGCAAA	TTTGCGACAGTGTTGCTGAGACCG
597	CGAACGTTCTCCGATGTAATGGCC	GGCCATTACATCGGAGAACGTTCG
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601	ACTCGAACGGACGTTCAATTCCCA	TGGGAATTGAACGTCCGTTCGAGT
602	CTGCATGGTGTGGGTGAGACTCCC	GGGAGTCTCACCCACACCATGCAG
603	CCGCGAGTGTGGATGGCGTGTTGA	TCAACACGCCATCCACACTCGCGG
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606	GGCGTGGGAGGATAAGACGATGTC	GACATCGTCTTATCCTCCCACGCC
607	TGCTCCATGTTAGGAACGCACCAC	GTGGTGCGTTCCTAACATGGAGCA
608	CGGTGTTGGTCGGACTGACGACTG	CAGTCGTCAGTCCGACCAACACCG
609	CCGCGCGTATCTATCAGATCTGGG	CCCAGATCTGATAGATACGCGCGG
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612	TGCTTACGCAGTGGATTGGTCAGA	TCTGACCAATCCACTGCGTAAGCA
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615	AGGGTTCCTTACGCGTCGACATGG	CCATGTCGACGCGTAAGGAACCCT
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617	TCGTAGTCTCACCGGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
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623	CGACTCGCTGGACAGGAGAATCGT	ACGATTCTCCTGTCCAGCGAGTCG
624	CATGATCCTCTGTTTCACCCGCGG	CCGCGGGTGAAACAGAGGATCATG
625	GGCGTAGCGCTCTAAAAGCTTCGG	CCGAAGCTTTTAGAGCGCTACGCC
626	AGTGATGCCATCAGGCCCGTATAC	GTATACGGGCCTGATGGCATCACT
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630	CAGGCCCGAACCACGCGGTTACAG	CTGTAACCGCGTGGTTCGGGCCTG
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633	GATGGTGGACTGGAGCCCTTCCGC	GCGGAAGGGCTCCAGTCCACCATC
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635	TCTTCTGGCTGTCCGGCACCCGAA	TTCGGGTGCCGGACAGCCAGAAGA
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641	GTGCTTGACGAAGAGGCGAAATGT	ACATTTCGCCTCTTCGTCAAGCAC
642	CAGTCCGTGCGCTTCATGTCCTCA	TGAGGACATGAAGCGCACGGACTG
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644	GGCGAGTCTTGTGGGGACATGTGT	ACACATGTCCCCACAAGACTCGCC
645	CCAAAGCGAAGCGAGCGTGTCTAT	ATAGACACGCTCGCTTCGCTTTGG
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647	AAATCCGCGATGTGCCGTGAGGCT	AGCCTCACGGCACATCGCGGATTT
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686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGGAGGCTACCAGCTGACA
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690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGCAGAATGCGAC
691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
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709	AACAGGATATCCGCGATCACGACA	TGTCGTGATCGCGGATATCCTGTT
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746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
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769	ATAGGTAGGATGTGCCCGGCGTTG	CAACGCCGGGCACATCCTACCTAT
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771	CTGGCTGTGTCGCATCTCGTTAAC	GTTAACGAGATGCGACACAGCCAG
772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
773	TTTTCATAAACGTTGTCCCCGAGC	GCTCGGGGACAACGTTTATGAAAA
774	AGCAGGAGGACGAACCTCCGCTCC	GGAGCGGAGGTTCGTCCTCCTGCT
775	TTCAAGCACCATCGTGCAATCCAA	TTGGATTGCACGATGGTGCTTGAA

776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
777	TACATTCCCTGCCTCCGTGGGCTT	AAGCCCACGGAGGCAGGGAATGTA
778	CGCTTCGCGTATTCAGTAGCGGTT	AACCGCTACTGAATACGCGAAGCG
779	TCGGACGCGTCGACACTCATTATA	TATAATGAGTGTCGACGCGTCCGA
780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCCTGCTCAGA
781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAGGGCTTGGCAATTCAA
782	AGTTTTCGCCTTGATGCGTCGGTG	CACCGACGCATCAAGGCGAAAACT
783	GTTTCATAGGCCACGCGTGCTAAA	TTTAGCACGCGTGGCCTATGAAAC
784	GGAGCGAAGACTTCGTCTGCCCAA	TTGGGCAGACGAAGTCTTCGCTCC
785	ATTGGCCGAGGGTGAATGCAGCCT	AGGCTGCATTCACCCTCGGCCAAT
786	TGATCCATCCGAATGCTTTTCCAT	ATGGAAAAGCATTCGGATGGATCA
787	GCACACAGTTGTCTTGGCCCATGA	TCATGGGCCAAGACAACTGTGTGC
788	CTGGCGGGCAGTGGAAAAAACAAC	GTTGTTTTTTCCACTGCCCGCCAG
789	ATCTCCATGCGTAAGACTGCTCCG	CGGAGCAGTCTTACGCATGGAGAT
790	TCTCCTCTCGTCGCAGTTCGTGGA	TCCACGAACTGCGACGAGAGGAGA
791	TAGCGTATTCACTCTTGCCGAGCA	TGCTCGGCAAGAGTGAATACGCTA
792	CAATCAAAAGCCACGGCGCGATGG	CCATCGCGCCGTGGCTTTTGATTG
793	AGCGTCACGGAATTCAGCAGATCT	AGATCTGCTGAATTCCGTGACGCT
794	GACTCCCTGTTAATGCGCCCAAGG	CCTTGGGCGCATTAACAGGGAGTC
795	TAGGCACTGCCGGTTCAGATTCAA	TTGAATCTGAACCGGCAGTGCCTA
796	AACAGGGTGATAACGGTGGCCAAT	ATTGGCCACCGTTATCACCCTGTT
797	CGTGCGTACCATGTGTAAGTGCGT	ACGCACTTACACATGGTACGCACG
798	GACCAATTCTACTTCGGCAGCCCA	TGGGCTGCCGAAGTAGAATTGGTC
799	ATCGGACCGATTTGCTTTTGGCTG	CAGCCAAAAGCAAATCGGTCCGAT
800	TCCGCCGAAGCACACGCTTATTCG	CGAATAAGCGTGTGCTTCGGCGGA
801	AACGGTACGCATTGTGAGCAGTGT	ACACTGCTCACAATGCGTACCGTT
802	TGGCGACTACTGTTCCCCTGAATC	GATTCAGGGGAACAGTAGTCGCCA
803	CAGAGGGGACAGCCGTATGCCTTA	TAAGGCATACGGCTGTCCCCTCTG
804	CGGTGGTTTTATCGGAATCTGCGA	TCGCAGATTCCGATAAAACCACCG
805	TTGGCCTCCGACCTCACGACATAT	ATATGTCGTGAGGTCGGAGGCCAA
806	CGTTTCGCTAGCATCTGGCGCCGA	TCGGCGCCAGATGCTAGCGAAACG
807	ACTAAGCGGTGGAGCCGGTGGATG	CATCCACCGGCTCCACCGCTTAGT
808	ATATTGGCTGCGTTTACGGGCCGC	GCGGCCCGTAAACGCAGCCAATAT
809	CCGCTATGGTGGCAATCCCGATAC	GTATCGGGATTGCCACCATAGCGG
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811	ATTCTGGGGAGTGACCCAGGGCTT	AAGCCCTGGGTCACTCCCCAGAAT
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813	GAAAGGACGGGATTTGGGGGCTAA	TTAGCCCCCAAATCCCGTCCTTTC
814	TATGTAGTACCTTGGCTCGCGCCA	TGGCGCGAGCCAAGGTACTACATA
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822	GATAGTGCTCGCAAACGGGCCTTC	GAAGGCCCGTTTGCGAGCACTATC
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824	GGCGTGAATAGAGTGACCAGGCGG	CCGCCTGGTCACTCTATTCACGCC
825	ACGTGCCAGCTGCGGGCACTTTAT	ATAAAGTGCCCGCAGCTGGCACGT
826	AGTGGAATAGTCGCGTCGTGCCGC	GCGGCACGACGCGACTATTCCACT
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835	CGTATCATAGCGTTCGGTGGACAA	TTGTCCACCGAACGCTATGATACG
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841	GGCCGCGGATTTTATTCCTTGGAT	ATCCAAGGAATAAAATCCGCGGCC
842	GAATTTGGAACGGTGTTCCGATGA	TCATCGGAACACCGTTCCAAATTC
843	GTCCATCCATCTACGGCATCAGGA	TCCTGATGCCGTAGATGGATGGAC
844	TAAACGACCTGGCACATGTGCGTA	TACGCACATGTGCCAGGTCGTTTA
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848	TGGGGTTCGTACAGGTCGGTTCAT	ATGAACCGACCTGTACGAACCCCA
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852	GGGACATGCGTAGCGCAATATCAC	GTGATATTGCGCTACGCATGTCCC
853	CACACGTCACACCATCCAAAGTGG	CCACTTTGGATGGTGTGACGTGTG
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858	GTCGGCGCAGCCGATCCTCATGTC	GACATGAGGATCGGCTGCGCCGAC
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860	ATCTCTTCCTCGGGTGGATGCCAG	CTGGCATCCACCCGAGGAAGAGAT
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862	GTTAAGGGGTGAGAACATCCGGCC	GGCCGGATGTTCTCACCCCTTAAC
863	AAGTCGTCTCCCTGCGTCTCGTCC	GGACGAGACGCAGGGAGACGACTT
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865	CATCATTGGCACCGTACCAATGCC	GGCATTGGTACGGTGCCAATGATG
866	TGGAGAAAGGGAAGTGCAGCAACG	CGTTGCTGCACTTCCCTTTCTCCA
867	TGGTACTCCTTGTCATGCCTGCCA	TGGCAGGCATGACAAGGAGTACCA
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872	TCGAGCACGGTCACTGATAAAGCC	GGCTTTATCAGTGACCGTGCTCGA
873	GAGGGTCCCTGCTCAGAGTTGGTT	AACCAACTCTGAGCAGGGACCCTC
874	AAATGCGATCGCCCCTTATGGAAT	ATTCCATAAGGGGCGATCGCATTT
875	CTACCCGAATGGATTGCGGATGGC	GCCATCCGCAATCCATTCGGGTAG
876	AGGGACTGGCAGGTCTCTGCGCGT	ACGCGCAGAGACCTGCCAGTCCCT
877	TAACGATCCATTCCACGAATGCAG	CTGCATTCGTGGAATGGATCGTTA
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881	CCGAAGGTTTCACGCTCAGGTCGC	GCGACCTGAGCGTGAAACCTTCGG
882	GAACCCAGCTGGGACATCCTTCAG	CTGAAGGATGTCCCAGCTGGGTTC
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884	AATTGTCCGCCAAACGCTTTTCAG	CTGAAAAGCGTTTGGCGGACAATT
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886	TCGCGTGCTCTACGTAGCCCATGA	TCATGGGCTACGTAGAGCACGCGA
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892	CCCCACACGTTGCGCCTATATGTG	CACATATAGGCGCAACGTGTGGGG
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905	GTGGGTTTTGTTCACCCTTCTGGG	CCCAGAAGGGTGAACAAAACCCAC
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908	GTGAAATGGATCCAGAGAGGGCCA	TGGCCCTCTCTGGATCCATTTCAC
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911	GGGTTCTAGCGTGCGCGTTCAGTT	AACTGAACGCGCACGCTAGAACCC
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913	CCGTCTTCAGGACAACGGTATGCG	CGCATACCGTTGTCCTGAAGACGG
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918	CAAACCACAGCTTACAGGCTGCGT	ACGCAGCCTGTAAGCTGTGGTTTG
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922	CGCTTAACGGCATTGACTGTCCAC	GTGGACAGTCAATGCCGTTAAGCG
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943	CAAGCGTGGAAGTACGACCCGCCA	TGGCGGGTCGTACTTCCACGCTTG
944	GTGTGCACTGGATCCGAGCCCTAG	CTAGGGCTCGGATCCAGTGCACAC
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1062	ACAGGCACGTAAGTGCTCAATCGG	CCGATTGAGCACTTACGTGCCTGT

1063	AGCAAGATAGCGGGAGTGCCCCTA	TAGGGGCACTCCCGCTATCTTGCT
1064	GGTTTACGCCATGACATCCCGTCA	TGACGGGATGTCATGGCGTAAACC
1065	GTGCAGGCCTTTGTGTGTGAATCG	CGATTCACACACAAAGGCCTGCAC
1066	CTTCGAGGGTAGGGCTTCGAAACG	CGTTTCGAAGCCCTACCCTCGAAG
1067	AGTCGACACTTGGGTTTACCACGG	CCGTGGTAAACCCAAGTGTCGACT
1068	ACATAAATCTCGCCCGCTGCACTC	GAGTGCAGCGGGCGAGATTTATGT
1069	GTTTGGTTTTCCACGGAGGTTTGA	TCAAACCTCCGTGGAAAACCAAAC
1070	GCAGGAACCAGATTAGTGTCCCGG	CCGGGACACTAATCTGGTTCCTGC
1071	TTTGCTAGAGCGCGGAGCTAAAGC	GCTTTAGCTCCGCGCTCTAGCAAA
1072	CTATGTGGCATCGCTGACATGCTC	GAGCATGTCAGCGATGCCACATAG
1073	CCTAAGTCGGTTTGCAGCTGCTCT	AGAGCAGCTGCAAACCGACTTAGG
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1075	TAACCCGCGCCCGAGAAATTGTCT	AGACAATTTCTCGGGCGCGGGTTA
1076	TATGGTGCTCAGAGCTGTTGCCAA	TTGGCAACAGCTCTGAGCACCATA
1077	TCATCGACCCACTAACGTCAGGGC	GCCCTGACGTTAGTGGGTCGATGA
1078	TGCTCAAGCTACGCGTCACTTCCC	GGGAAGTGACGCGTAGCTTGAGCA
1079	AGCGGGAAGGTCTGAGGAGGGAAA	TTTCCCTCCTCAGACCTTCCCGCT
1080	CCGATGTAGCACCACCGCAGTGGC	GCCACTGCGGTGGTGCTACATCGG
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1082	CACCAGCCTTACGTGCGGCGTTAA	TTAACGCCGCACGTAAGGCTGGTG
1083	CGTTTCGCCTCCTCTTCCGAATGC	GCATTCGGAAGAGGAGGCGAAACG
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1086	TGAGGACAAACCGCGCGTAGGATA	TATCCTACGCGCGGTTTGTCCTCA
1087	TCGTAGAGACGCAGTGCCCATCTC	GAGATGGGCACTGCGTCTCTACGA
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1091	GGTGTGCTTTTACGCATGTACGCA	TGCGTACATGCGTAAAAGCACACC
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1093	AAATTAGGCACAGCCCTCCCACAG	CTGTGGGAGGGCTGTGCCTAATTT
1094	ATAAGTTTGGTGAGCCATTCGCGA	TCGCGAATGGCTCACCAAACTTAT
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1097	CCTCTCGGACGGTCCCTTTGATCG	CGATCAAAGGGACCGTCCGAGAGG
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1103	AGACGCGTACGAGGGTTCTGCGCC	GGCGCAGAACCCTCGTACGCGTCT

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1107	CTTATCCCATGTGCCGGTCTGACT	AGTCAGACCGGCACATGGGATAAG
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1124	GACATTTAACCCGACCGATTGTGC	GCACAATCGGTCGGGTTAAATGTC
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1126	CTCAAGCGTGCATGTTGGTAACCA	TGGTTACCAACATGCACGCTTGAG
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1132	TGCTAGACCCAGCCCGAGTCTCGG	CCGAGACTCGGGCTGGGTCTAGCA
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1138	ACCTGTGCAGTCAGCACGAGTGCG	CGCACTCGTGCTGACTGCACAGGT
1139	GAGAACCACAGGTGGTCCACCCTA	TAGGGTGGACCACCTGTGGTTCTC
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1350	GGAGTGACCAGCACAAGCATCGAG	CTCGATGCTTGTGCTGGTCACTCC
1351	TCGGACTGGAAGTAACTCGCATGA	TCATGCGAGTTACTTCCAGTCCGA
1352	GTAGGGTCAAGCACGATTGAAGCC	GGCTTCAATCGTGCTTGACCCTAC
1353	CACCGGCGGTTCGACTAACGTGAC	GTCACGTTAGTCGAACCGCCGGTG
1354	GAATGACGCGCAGTGCATTTGAAC	GTTCAAATGCACTGCGCGTCATTC
1355	GTGCTCGTCTAACCGCGGATAGAG	CTCTATCCGCGGTTAGACGAGCAC
1356	GCGGACCTGGGTTAATTGACGCGC	GCGCGTCAATTAACCCAGGTCCGC
1357	TTTTTGATGTTGCGCACCGGGCTA	TAGCCCGGTGCGCAACATCAAAAA
1358	TTGCGTCAGCGCATCTGCTCGATT	AATCGAGCAGATGCGCTGACGCAA
1359	ATGAGCACGCCAGTTCGTTCCTTT	AAAGGAACGAACTGGCGTGCTCAT
1360	TCAACGGTAAAGAATCGCCCCGCA	TGCGGGGCGATTCTTTACCGTTGA
1361	CGCGATTGACTGAACCACACCTCT	AGAGGTGTGGTTCAGTCAATCGCG
1362	GCGTGAAAGATGACGGCCGGTATA	TATACCGGCCGTCATCTTTCACGC
1363	CATGATTCCACCTCGATCGGCTAG	CTAGCCGATCGAGGTGGAATCATG
1364	CTACGACAAAGCAACCGTGCAAAA	TTTTGCACGGTTGCTTTGTCGTAG
1365	ATGCCGTGTTCATCTTGATGGTCC	GGACCATCAAGATGAACACGGCAT
1366	TTCGTGGAGGGACTTTGGAGATCC	GGATCTCCAAAGTCCCTCCACGAA
1367	GAAGCGCCGTAACGTACACCGTCG	CGACGGTGTACGTTACGGCGCTTC
1368	AGCGTGCGCTTGGCTATAAGGCTA	TAGCCTTATAGCCAAGCGCACGCT
1369	ACAGTCAGGAGTAACGCCGCTCAA	TTGAGCGGCGTTACTCCTGACTGT
1370	TTTAGCCGCTGCGACTGTAGGAAA	TTTCCTACAGTCGCAGCGGCTAAA
1371	ACTGTGTCGCAATCAACCCGCAAA	TTTGCGGGTTGATTGCGACACAGT
1372	TGCAGCCAATGCGGAACTTAGAGG	CCTCTAAGTTCCGCATTGGCTGCA
1373	CCCGCTATCCCGGTCTTGCAGTTC	GAACTGCAAGACCGGGATAGCGGG
1374	GAGGGCGCAACATATGCAGTGCTG	CAGCACTGCATATGTTGCGCCCTC
1375	CGTACGGACATCGATGACGCAACG	CGTTGCGTCATCGATGTCCGTACG
1376	AGTCTCCCGAGAAACGCATAAGGC	GCCTTATGCGTTTCTCGGGAGACT
1377	AGGAAGTGGATGAACGCGGCTGCA	TGCAGCCGCGTTCATCCACTTCCT
1378	GGGTTGCTCACCCTCGTCATCAGG	CCTGATGACGAGGGTGAGCAACCC
1379	TAGGAATGCGAGTTCCGGCGGTAA	TTACCGCCGGAACTCGCATTCCTA
1380	CTCCTCACTTCCAAGCTGCGGATA	TATCCGCAGCTTGGAAGTGAGGAG
1381	TCAATAGCACCTAGCATGCTCCCG	CGGGAGCATGCTAGGTGCTATTGA
1382	TGATTCCTGCGCTTTCACAGGTCG	CGACCTGTGAAAGCGCAGGAATCA
1383	GTATGTGCGGGATGGAAATCACGC	GCGTGATTTCCATCCCGCACATAC
1384	TACGGCAACTGTCGATACGAGGGC	GCCCTCGTATCGACAGTTGCCGTA
1385	GGTTCCCTATCCAGCACTCCTCGC	GCGAGGAGTGCTGGATAGGGAACC
1386	ATAAGCGCGCCACAGGTATGTACC	GGTACATACCTGTGGCGCGCTTAT
1387	GAAAGTCGCCAACAGACTCGAGCA	TGCTCGAGTCTGTTGGCGACTTTC
1388	CGCTAATGCCTCATAGGCGTGTGC	GCACACGCCTATGAGGCATTAGCG
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1390	GACGCTGCTGATGGCTTTATCGAT	ATCGATAAAGCCATCAGCAGCGTC

1391	CTCTCCCCGTCGCTTCAGAGATTA	TAATCTCTGAAGCGACGGGGAGAG
1392	TCATGTGGGCCGTCGTATCAGTTT	AAACTGATACGACGGCCCACATGA
1393	GGCCTGAAGGTGAATGGTTACGTG	CACGTAACCATTCACCTTCAGGCC
1394	AGCCTCCAAAGCCGGTAGAGTTCC	GGAACTCTACCGGCTTTGGAGGCT
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1396	GCCTGAGTCCGGGTCGGGAAAGAA	TTCTTTCCCGACCCGGACTCAGGC
1397	GGCACTATACCGGTTCTGGACGCG	CGCGTCCAGAACCGGTATAGTGCC
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1399	CCCAAGGCAAGTGTGCATCAGTCC	GGACTGATGCACACTTGCCTTGGG
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1403	TTGGCACTCTGCAAGATACGTGGG	CCCACGTATCTTGCAGAGTGCCAA
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1405	CGATCAACTTGCGGCCATTCCTGC	GCAGGAATGGCCGCAAGTTGATCG
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1407	GCGGCTAGTTGTACCTAGCGGCTG	CAGCCGCTAGGTACAACTAGCCGC
1408	TCGTCACTGTTAGAGAGGCCTCCG	CGGAGGCCTCTCTAACAGTGACGA
1409	AGTGTCGTGAGCCCTAGCGGCGCT	AGCGCCGCTAGGGCTCACGACACT
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1411	ACCGATGCGCGGTCGGTCTCATAC	GTATGAGACCGACCGCGCATCGGT
1412	GGCAGAGGGTTAGGGGGTTTTTTT	AAAAAAACCCCCTAACCCTCTGCC
1413	GGCAAAGGGTGTTTATGGGAGACC	GGTCTCCCATAAACACCCTTTGCC
1414	ACAAGGCTTCGGCTGGCAGAATAC	GTATTCTGCCAGCCGAAGCCTTGT
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1418	GTTCAGCAGTAGCTCCCTCCTCGA	TCGAGGAGGGAGCTACTGCTGAAC
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1420	ACGATCCATTTTGCCAGCATGCAA	TTGCATGCTGGCAAAATGGATCGT
1421	TCCCTTCATTTCGGGTTTTTAGCC	GGCTAAAAACCCGAAATGAAGGGA
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1424	GACCCTCACGGTCATCAGAGGGAG	CTCCCTCTGATGACCGTGAGGGTC
1425	CCGTTCAACACAGTGATACACGCG	CGCGTGTATCACTGTGTTGAACGG
1426	CACCAGGGGATAGGTGCGGTACGC	GCGTACCGCACCTATCCCCTGGTG
1427	GGTCGGAACTGATCTGTGCGATCC	GGATCGCACAGATCAGTTCCGACC
1428	TGCTCCTTCCTAGGGTCATCCGTG	CACGGATGACCCTAGGAAGGAGCA
1429	GTGGACTTTGACGCCGGCTACCGC	GCGGTAGCCGGCGTCAAAGTCCAC
1430	CTGATCTGTCGGCGGTTACTTGCC	GGCAAGTAACCGCCGACAGATCAG
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1434	GGCGCACTCCAATACCCACTGTTT	AAACAGTGGGTATTGGAGTGCGCC
1435	GCGCTTGGAGACTGTCAGGACGTG	CACGTCCTGACAGTCTCCAAGCGC
1436	CAAACCGCTGGTTTCTCCACCTGT	ACAGGTGGAGAAACCAGCGGTTTG
1437	GCGATTGCTTGGGATCGGTGACTA	TAGTCACCGATCCCAAGCAATCGC
1438	CTCAGCGACATTTTTCTGGTGGCG	CGCCACCAGAAAAATGTCGCTGAG
1439	CAGCGGCGTCGTTTACTCAGGACT	AGTCCTGAGTAAACGACGCCGCTG
1440	GACAGCCGTGAACGCTCAGCCGTT	AACGGCTGAGCGTTCACGGCTGTC
1441	GGGCCGTAGAGGCATCGGGTAAAG	CTTTACCCGATGCCTCTACGGCCC
1442	CGCCGCTCACCTGCTTAAAGCATT	AATGCTTTAAGCAGGTGAGCGGCG
1443	TGCCAAATCGCAACTCTTGAGACA	TGTCTCAAGAGTTGCGATTTGGCA
1444	CCCCGATCGGGTGTAATTCTCCCT	AGGGAGAATTACACCCGATCGGGG
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1446	CGAGCCTTCAGTGGTATGCATGCG	CGCATGCATACCACTGAAGGCTCG
1447	CAGCAGCGTGCCCATCTCGACTTA	TAAGTCGAGATGGGCACGCTGCTG
1448	CGGACCAAGATGGCAGTAATCCAG	CTGGATTACTGCCATCTTGGTCCG
1449	CTACCACGCTCTGCGCGGGCTGTA	TACAGCCCGCGCAGAGCGTGGTAG
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1451	CGACATATCCGACATGACCGGATG	CATCCGGTCATGTCGGATATGTCG
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1459	ACTGCATAGCCCAGATCCGCTTGC	GCAAGCGGATCTGGGCTATGCAGT
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1472	GGAAAGTTGGCGGATCCGAGCACT	AGTGCTCGGATCCGCCAACTTTCC

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1475	CTCGCCTTAGATCGTGGTTCCGCA	TGCGGAACCACGATCTAAGGCGAG
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1636	CATGCCTGAACAATCTCGCATCCC	GGGATGCGAGATTGTTCAGGCATG

1637	GAGCCTGGCTCCACAGCTGTGCTC	GAGCACAGCTGTGGAGCCAGGCTC
1638	CTTTCGATACCATCGTTGGCGATC	GATCGCCAACGATGGTATCGAAAG
1639	CCCGGAGGTGAGGCATTGAATATG	CATATTCAATGCCTCACCTCCGGG
1640	CTCATTCAGCTAAAAGCGGCTGGA	TCCAGCCGCTTTTAGCTGAATGAG
1641	GAAATGCCCTGGGGACTTTTTGCC	GGCAAAAAGTCCCCAGGGCATTTC
1642	TTTGCCTTCACAACAGACGCAGCA	TGCTGCGTCTGTTGTGAAGGCAAA
1643	AAATCCCAAGACGTCGGGGCGTAT	ATACGCCCCGACGTCTTGGGATTT
1644	CAACGGGCGGTAGCTAAACCGTAA	TTACGGTTTAGCTACCGCCCGTTG
1645	GGCCAACGACAATGCGAAACCTTC	GAAGGTTTCGCATTGTCGTTGGCC
1646	GACATCACGCAAAATCTCAGCGCA	TGCGCTGAGATTTTGCGTGATGTC
1647	ACGTTCCGTCCACAACCGTATGTT	AACATACGGTTGTGGACGGAACGT
1648	GCTCATAGGTCTTCCGTAGCCCGT	ACGGGCTACGGAAGACCTATGAGC
1649	GAAACGAGTCTCTCGCGCCCTAGA	TCTAGGGCGCGAGAGACTCGTTTC
1650	CGGGACAGAAGCAAGTTACATCGG	CCGATGTAACTTGCTTCTGTCCCG
1651	TGACCGCTCGATACCAGGAGGGTG	CACCCTCCTGGTATCGAGCGGTCA
1652	CTGGCAATAAAGACCTTCCGACCA	TGGTCGGAAGGTCTTTATTGCCAG
1653	TGCGCGACGTCATGTTGGTGATTA	TAATCACCAACATGACGTCGCGCA
1654	GTTGGTTGTGGGAACACACCCGCT	AGCGGGTGTGTTCCCACAACCAAC
1655	TGTGGGTTCGGAAACACAGGAAGT	ACTTCCTGTGTTTCCGAACCCACA
1656	GGAAAAAACGGCAATTAGCCGAGT	ACTCGGCTAATTGCCGTTTTTTCC
1657	TGGTGCGGAGTGCCCTCTATTGGG	CCCAATAGAGGGCACTCCGCACCA
1658	AACCAACAGGCTGCAGCCCAGACT	AGTCTGGGCTGCAGCCTGTTGGTT
1659	AAACAGATCCATCTGCACGCCAGG	CCTGGCGTGCAGATGGATCTGTTT
1660	GGAATACCGCGGCGATTATGGCTT	AAGCCATAATCGCCGCGGTATTCC
1661	TACTGTTCGCGGCAAACCGTCACT	AGTGACGGTTTGCCGCGAACAGTA
1662	GATCTCTCGTGGAGCACGTTTTCC	GGAAAACGTGCTCCACGAGAGATC
1663	GGCATAGCAAACCTTGACCTCCAA	TTGGAGGTCAAGGTTTGCTATGCC
1664	ATCTGGGATTCGCGAGCCAATATC	GATATTGGCTCGCGAATCCCAGAT
1665	CGATCAGGATATCATTTACGCCCG	CGGGCGTAAATGATATCCTGATCG
1666	ACGGTACCGAAACGGTCTCAGCGT	ACGCTGAGACCGTTTCGGTACCGT
1667	CTCCCATACCTGCGTTCTTACCGA	TCGGTAAGAACGCAGGTATGGGAG
1668	GCACGAGAACCTAATTGTCGCACA	TGTGCGACAATTAGGTTCTCGTGC
1669	GCCACACGATCAAGACAGCGCATG	CATGCGCTGTCTTGATCGTGTGGC
1670	CCCGTTAACTCACGAGCGGTCAAT	ATTGACCGCTCGTGAGTTAACGGG
1671	AGAGAAGGTCATTGCCTGTCGGTG	CACCGACAGGCAATGACCTTCTCT
1672	CGGGCCCTCTTAAAGTAGAGCAGG	CCTGCTCTACTTTAAGAGGGCCCG
1673	ACATCGCGTCCGAGGGAGTTAGCG	CGCTAACTCCCTCGGACGCGATGT
1674	AATGCCTAATCGAGCCAGCGGATC	GATCCGCTGGCTCGATTAGGCATT
1675	CTCGATCTTTTTAAACCGGCGCTT	AAGCGCCGGTTTAAAAAGATCGAG
1676	CGTTCCTGGAAGGCAGGGTCTCAC	GTGAGACCCTGCCTTCCAGGAACG
1677	CCTGTGCTTACTATCGGCGATCCA	TGGATCGCCGATAGTAAGCACAGG

1678	GTTAGTCGCCCTATTGGCCTGGTT	AACCAGGCCAATAGGGCGACTAAC
1679	CCGGTGAGATGACTGTAAATGCCA	TGGCATTTACAGTCATCTCACCGG
1680	CGTGGTTTAAAACATCGCGCTTCG	CGAAGCGCGATGTTTTAAACCACG
1681	TAAGACGCAGAAGATGGGGTCCAC	GTGGACCCCATCTTCTGCGTCTTA
1682	CACCACAGCTTCTTTGTTCGACCC	GGGTCGAACAAAGAAGCTGTGGTG
1683	TCGGGTCCGTACCACCACTTTTGC	GCAAAAGTGGTGGTACGGACCCGA
1684	CCAAGCCCCGAGTACCGAAGATTT	AAATCTTCGGTACTCGGGGCTTGG
1685	TCCGTGATATGGTCGTGGCGCGGT	ACCGCGCCACGACCATATCACGGA
1686	TGTCTGTGTCATGGCACCTCGCAT	ATGCGAGGTGCCATGACACAGACA
1687	AGGACTGCACTGTGCACGTCTGAT	ATCAGACGTGCACAGTGCAGTCCT
1688	CCATCCTCATGTACAGCGCCGCTG	CAGCGGCGCTGTACATGAGGATGG
1689	GTACCCGCGCCTTCCTCGACACAG	CTGTGTCGAGGAAGGCGCGGGTAC
1690	ACGGGTCCTGGTCGACTAAGGCTT	AAGCCTTAGTCGACCAGGACCCGT
1691	CGTATCGAAGGCGTGTACAACCGG	CCGGTTGTACACGCCTTCGATACG
1692	TGCCCGCCCTTTATGCAACGCTCA	TGAGCGTTGCATAAAGGGCGGGCA
1693	AAACTTACGAGACGGCGGCTGCCA	TGGCAGCCGCCGTCTCGTAAGTTT
1694	AAGTCTGACAAACGGAACGGGTGT	ACACCCGTTCCGTTTGTCAGACTT
1695	TAAGCGCAGACCAAAGTATGCGGC	GCCGCATACTTTGGTCTGCGCTTA
1696	GCAGTTTTTCAGATCCTCCGCAAA	TTTGCGGAGGATCTGAAAAACTGC
1697	TCGGAAGCATTTACGCGATCTCAG	CTGAGATCGCGTAAATGCTTCCGA
1698	CACAGAAACGGTTGAACGAACGCC	GGCGTTCGTTCAACCGTTTCTGTG
1699	GCATGCTCAGATGGTCGTGCTCAC	GTGAGCACGACCATCTGAGCATGC
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1702	ATTATTACGGGACCGAACCAACGG	CCGTTGGTTCGGTCCCGTAATAAT
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1704	GACATTCGTGACTTGGTCGTCCGC	GCGGACGACCAAGTCACGAATGTC
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1706	GAGTTGTGCGGAGTCATCGGAGTC	GACTCCGATGACTCCGCACAACTC
1707	GCCTTTACAGATTTGGCGGGCTAT	ATAGCCCGCCAAATCTGTAAAGGC
1708	ATGGCGTTTGCGAAGTCGATACAG	CTGTATCGACTTCGCAAACGCCAT
1709	TGCATCGGCCTCAATCAGAGAACT	AGTTCTCTGATTGAGGCCGATGCA
1710	ACAATCATGGCAATCTGGCAAATG	CATTTGCCAGATTGCCATGATTGT
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1712	AGGGCAGGGGACGGACAGTAAGTC	GACTTACTGTCCGTCCCCTGCCCT
1713	GCATAGGGCGAATCTAGTACGGGC	GCCCGTACTAGATTCGCCCTATGC
1714	TCCGGCGCATCCTCATTAGCAACT	AGTTGCTAATGAGGATGCGCCGGA
1715	TGGCCGCTTCCACTAATATTGGAC	GTCCAATATTAGTGGAAGCGGCCA
1716	CCGGCGGACGGCTCTTGTCAATGA	TCATTGACAAGAGCCGTCCGCCGG
1717	CGAGCAACCCAAAAGGAAGCAGTA	TACTGCTTCCTTTTGGGTTGCTCG
1718	GCGTATGATTCGGCAATCCGCCAG	CTGGCGGATTGCCGAATCATACGC

1719	AGTACCGCTACAACGCTGGTTCGC	GCGAACCAGCGTTGTAGCGGTACT
1720	GGGCAGGCCAGGTCCACCTGAGAA	TTCTCAGGTGGACCTGGCCTGCCC
1721	CCACTTCTGTGACCGAACCGTGCT	AGCACGGTTCGGTCACAGAAGTGG
1722	CCTGGTACCAGGCAGCAGTTGATT	AATCAACTGCTGCCTGGTACCAGG
1723	TTAGGGTACCGTCGAGAGACGCCA	TGGCGTCTCTCGACGGTACCCTAA
1724	GGTTGCTTGTGCGCGTGAGGTAGT	ACTACCTCACGCGCACAAGCAACC
1725	TGCTTCGACCGATGAAACTCGAAG	CTTCGAGTTTCATCGGTCGAAGCA
1726	TGCCACCCATACTATGCCCAGTGG	CCACTGGGCATAGTATGGGTGGCA
1727	TGTGCGGCAACGCGTGAAGACGTT	AACGTCTTCACGCGTTGCCGCACA
1728	TGAGAGAAGCTGGCCTCGGATCAG	CTGATCCGAGGCCAGCTTCTCTCA
1729	TATTGCGAATTCGAGTACGTGCCC	GGGCACGTACTCGAATTCGCAATA
1730	CGAGAGGGGTTCCCCAGTGATCGA	TCGATCACTGGGGAACCCCTCTCG
1731	TGCCTGGGGTGTCGTTCTAATTCT	AGAATTAGAACGACACCCCAGGCA
1732	GTGCGTCATTGTGGGTCATCCCAA	TTGGGATGACCCACAATGACGCAC
1733	AGGGCTCCCAGCATACCAACGTTG	CAACGTTGGTATGCTGGGAGCCCT
1734	AACTAGCCGCACCTTTGTGCAGAG	CTCTGCACAAAGGTGCGGCTAGTT
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1736	CGGCCTCGGTTGTACGGGTAGTCT	AGACTACCCGTACAACCGAGGCCG
1737	TCTTTGAGGCGCGGACCCGCATAT	ATATGCGGGTCCGCGCCTCAAAGA
1738	GATGGTTCGCCCTTGTGTCGCAGC	GCTGCGACACAAGGGCGAACCATC
1739	GAGATTCAATACAGGCCGCGGGTC	GACCCGCGGCCTGTATTGAATCTC
1740	AGGGCGAAGGAAGGTTCCGTTTTT	AAAAACGGAACCTTCCTTCGCCCT
1741	CTCGACCCCTGCCACTACTGGTTC	GAACCAGTAGTGGCAGGGGTCGAG
1742	TGTTCCGCGGTCTACGCATTACTG	CAGTAATGCGTAGACCGCGGAACA
1743	GAGACGACGTCCTACACCCGCTAA	TTAGCGGGTGTAGGACGTCGTCTC
1744	AGATTGCGACAGCGACACGTGATT	AATCACGTGTCGCTGTCGCAATCT
1745	GATACCGTTGGGCATTTCTCGGTA	TACCGAGAAATGCCCAACGGTATC
1746	GATTGGGAGGCATTCAGCGACGGA	TCCGTCGCTGAATGCCTCCCAATC
1747	AGGAGGAAACGAGGGCGTAGGTTC	GAACCTACGCCCTCGTTTCCTCCT
1748	GCCAAACAACGTCTGACGCCTAGC	GCTAGGCGTCAGACGTTGTTTGGC
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1750	TTATCGGCCGTTAAAATGGGATGG	CCATCCCATTTTAACGGCCGATAA
1751	CCTTGGATTCGTTCATCGCTAGCA	TGCTAGCGATGAACGAATCCAAGG
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1753	TCCTTACCCCTCGTTCAAACGCCT	AGGCGTTTGAACGAGGGGTAAGGA
1754	ATTCCTGAACCATGCATGGCCTGT	ACAGGCCATGCATGGTTCAGGAAT
1755	AGCGAGACGCTCGATCACGAACTA	TAGTTCGTGATCGAGCGTCTCGCT
1756	GCTGGTCTGGCTCGCTGTTTAGAA	TTCTAAACAGCGAGCCAGACCAGC
1757	CGTGCGCGGCATAAAGATAGGTCT	AGACCTATCTTTATGCCGCGCACG
1758	TCTGGCACTCACATCGGACAGTCT	AGACTGTCCGATGTGAGTGCCAGA
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1760	TCCAGGGTCGGAGTACATGGCGGG	CCCGCCATGTACTCCGACCCTGGA
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1762	TGCTGGCGTCAACACTTCCCGATT	AATCGGGAAGTGTTGACGCCAGCA
1763	CAGGGCGGTGCGGTGAACTAGCCA	TGGCTAGTTCACCGCACCGCCCTG
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1767	GGAGCCACACCAGTCGAAGATGGT	ACCATCTTCGACTGGTGTGGCTCC
1768	CGCCACCGGAAATTGAAAAGACTG	CAGTCTTTTCAATTTCCGGTGGCG
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1771	CGAACCAAGCTGCATTGTCAGTGG	CCACTGACAATGCAGCTTGGTTCG
1772	GAGTCTGCGCTTGCAATCTTTGCG	CGCAAAGATTGCAAGCGCAGACTC
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1791	GGAGTGGGTTCCGCGAATTCACTG	CAGTGAATTCGCGGAACCCACTCC
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1921	GGCTTACTCCTCAATTGCGACACG	CGTGTCGCAATTGAGGAGTAAGCC
1922	CACGACTCCCTGCCAGATTTGATT	AATCAAATCTGGCAGGGAGTCGTG
1923	CTTAGACGTCGGCAATGTCACGTC	GACGTGACATTGCCGACGTCTAAG

1924	CTCAGAGCACAATCTGCCCTGCCT	AGGCAGGGCAGATTGTGCTCTGAG
1925	GCTAGGAAAGTCGGCATTCATGGG	CCCATGAATGCCGACTTTCCTAGC
1926	AAAGCCCCAAAATTCCGCCTAACC	GGTTAGGCGGAATTTTGGGGCTTT
1927	GCGCAACGCTAAGGGACTATCAAG	CTTGATAGTCCCTTAGCGTTGCGC
1928	CGTCCGCTGGGATGAGTCTCCTGC	GCAGGAGACTCATCCCAGCGGACG
1929	ACAGGCCTCGTGATTGGTGTGGGT	ACCCACACCAATCACGAGGCCTGT
1930	CATTCTCCTTCCGGGACCACGCCT	AGGCGTGGTCCCGGAAGGAGAATG
1931	TCGGAGTTGACCAAGCTCAGTGCG	CGCACTGAGCTTGGTCAACTCCGA
1932	ACGCGCCACTGCAATTGCAAACAC	GTGTTTGCAATTGCAGTGGCGCGT
1933	AGTTCATGGAGCCGGCGTATTGTT	AACAATACGCCGGCTCCATGAACT
1934	ACGTTTAATGCGGGGCCCGCCTAC	GTAGGCGGGCCCCGCATTAAACGT
1935	TGAGGCTTTAGCCTACGCGCAGGT	ACCTGCGCGTAGGCTAAAGCCTCA
1936	CAGCGTTATGAGCGCGGAGTTTAT	ATAAACTCCGCGCTCATAACGCTG
1937	GTCCACGTGACCACGGATAGTTGG	CCAACTATCCGTGGTCACGTGGAC
1938	GATTATGCTCCTACGCCTGCTCCG	CGGAGCAGGCGTAGGAGCATAATC
1939	TCGTCAAGGGCATGATGTGTGGGA	TCCCACACATCATGCCCTTGACGA
1940	GATGGACCGCCAAAGACACCTTGA	TCAAGGTGTCTTTGGCGGTCCATC
1941	TACACGAGGATGGGGTCAAGCTTT	AAAGCTTGACCCCATCCTCGTGTA
1942	ACACGCACAAAACGTTTGAAAGGC	GCCTTTCAAACGTTTTGTGCGTGT
1943	GTTATCGTGGGCCGATGGTACTGA	TCAGTACCATCGGCCCACGATAAC
1944	ACATGACCGTATCCGCCTGCTTCG	CGAAGCAGGCGGATACGGTCATGT
1945	GAAGGCGAACCACTGAAACTACGC	GCGTAGTTTCAGTGGTTCGCCTTC
1946	TGACTTTTGCAACGGGTGGAACCA	TGGTTCCACCCGTTGCAAAAGTCA
1947	TGAATTCGTAGGTTTTGGGTGCGG	CCGCACCCAAAACCTACGAATTCA
1948	AGCATTTATGAAGCGGCCATTGCG	CGCAATGGCCGCTTCATAAATGCT
1949	TGCTCCTCGCGTTGGTACCGTGAG	CTCACGGTACCAACGCGAGGAGCA
1950	CGCAGCAAGAAACAGCAACTGTTG	CAACAGTTGCTGTTTCTTGCTGCG
1951	AGACGCTTGGAGTGAAAACTCGGA	TCCGAGTTTTCACTCCAAGCGTCT
1952	CATTCGTAGAATGCCCCAAATGGA	TCCATTTGGGGCATTCTACGAATG
1953	CCAGAAGGTTCGGGACCCGTCGTG	CACGACGGGTCCCGAACCTTCTGG
1954	GAGAAGCCGGTTCTCAGAGCACAT	ATGTGCTCTGAGAACCGGCTTCTC
1955	TTGCGTTGCAAGATATCTGGCCCG	CGGGCCAGATATCTTGCAACGCAA
1956	GGGTTGCATGTTCAGGCAAGACGA	TCGTCTTGCCTGAACATGCAACCC
1957	CTCACGAAGGTGACATATCACGCC	GGCGTGATATGTCACCTTCGTGAG
1958	GCCCGAGATACGGGTTCAAAAAGA	TCTTTTTGAACCCGTATCTCGGGC
1959	CATCTTCGCGCTTCTTCACTCCGC	GCGGAGTGAAGAAGCGCGAAGATG
1960	TTACACGGTAAGCGTACGGCCGCC	GGCGGCCGTACGCTTACCGTGTAA
1961	ACCTTCGGACAATGTGGCGTTCGC	GCGAACGCCACATTGTCCGAAGGT
1962	TGAATGGTTCTGCTAGGCCCACAC	GTGTGGGCCTAGCAGAACCATTCA
1963	CACGCCTGTCTGACATATGGATGC	GCATCCATATGTCAGACAGGCGTG
1964	CGCCTCAACCCAATCTGAGAACGT	ACGTTCTCAGATTGGGTTGAGGCG

1965	TTACGCTTACTGCGAGCTGGGTCC	GGACCCAGCTCGCAGTAAGCGTAA
1966	GGCTTGTGGGGCAATACGCATCTT	AAGATGCGTATTGCCCCACAAGCC
1967	CACTCTCCTTTGGATGCGGAACAA	TTGTTCCGCATCCAAAGGAGAGTG
1968	GACCAGCCATCACGTAACGGCCCT	AGGGCCGTTACGTGATGGCTGGTC
1969	AGGAACCGGATGTGGTTATGGAGC	GCTCCATAACCACATCCGGTTCCT
1970	ATCCATGGGCAACTGAGCCTATGC	GCATAGGCTCAGTTGCCCATGGAT
1971	GGAACAGCACTTGTTACCGCCCAC	GTGGGCGGTAACAAGTGCTGTTCC
1972	TGGCTCGCTTCAAGCCTGTTTGCT	AGCAAACAGGCTTGAAGCGAGCCA
1973	CAAACGTGAGGTCATGACCACCAT	ATGGTGGTCATGACCTCACGTTTG
1974	ACCGATGTCTTGAAGTCCGGAGGT	ACCTCCGGACTTCAAGACATCGGT
1975	CGAAAATGCATGATGATCTCCCCT	AGGGGAGATCATCATGCATTTTCG
1976	TTTGGTATTCTCGCTGCACCGTTG	CAACGGTGCAGCGAGAATACCAAA
1977	GCGTACTCAACCACATTCCCGACC	GGTCGGGAATGTGGTTGAGTACGC
1978	AGCAAACAACAGCGGTCCGAGCAT	ATGCTCGGACCGCTGTTGTTTGCT
1979	GGACTAGGAGCGGGGATAGCTGAG	CTCAGCTATCCCCGCTCCTAGTCC
1980	CCTTAACGAAAACCTGTCGACCGC	GCGGTCGACAGGTTTTCGTTAAGG
1981	CTCGATCGCATAAGCAAGAAACCG	CGGTTTCTTGCTTATGCGATCGAG
1982	CCCGTTGTTTGGGCGACAAAAAGT	ACTTTTTGTCGCCCAAACAACGGG
1983	CGGCGGCTCTCGCATGATCTCGTT	AACGAGATCATGCGAGAGCCGCCG
1984	CGGATGGAGAGGAGTCTACGTCCC	GGGACGTAGACTCCTCTCCATCCG
1985	CAGAACAATATCGTGCGTCAACCG	CGGTTGACGCACGATATTGTTCTG
1986	CCTTTGCGCGCTCCGAGTAAGGTA	TACCTTACTCGGAGCGCGCAAAGG
1987	GGAAACGGCACCTATCTGTCGTGA	TCACGACAGATAGGTGCCGTTTCC
1988	CGACCGACAAAACCAAATGCCGCC	GGCGGCATTTGGTTTTGTCGGTCG
1989	CCAAGGGTGTGGGAGCTGAAGAGA	TCTCTTCAGCTCCCACACCCTTGG
1990	TTAAGTGCGCATAGTCCTCGTGGG	CCCACGAGGACTATGCGCACTTAA
1991	GCCTGGTGGGGTAAGTCATGATGC	GCATCATGACTTACCCCACCAGGC
1992	GAGCAGCAGATTGATGCGCTTATG	CATAAGCGCATCAATCTGCTGCTC
1993	TGCGCCAACTTCCGGAATATTTGC	GCAAATATTCCGGAAGTTGGCGCA
1994	AACCCCATCATGAAATGCTCTCCG	CGGAGAGCATTTCATGATGGGGTT
1995	GTCCAACGGTACTGGCGTGATGTT	AACATCACGCCAGTACCGTTGGAC
1996	ACTCGGCTGATCGTGAGATGGTGA	TCACCATCTCACGATCAGCCGAGT
1997	ATTCGTGGGCGCATCTCGGAATGT	ACATTCCGAGATGCGCCCACGAAT
1998	TCCCGTCCTGTAATCCAGGGAACA	TGTTCCCTGGATTACAGGACGGGA
1999	CTTCGCTGCACCTACATTGCGCCA	TGGCGCAATGTAGGTGCAGCGAAG
2000	GCGTGTAGATGACTGTGCTTTGGG	CCCAAAGCACAGTCATCTACACGC
2001	CTATGGTATCGAGACATCGGCGGA	TCCGCCGATGTCTCGATACCATAG
2002	CCTCGTACTCCGTCGTATGCACAA	TTGTGCATACGACGGAGTACGAGG
2003	TGGTGCGTCCGTAGTGCCTGCACT	AGTGCAGGCACTACGGACGCACCA
2004	CGCGATCCTAGTTGAAAGCTTTGC	GCAAAGCTTTCAACTAGGATCGCG
2005	ACGATCCAGGTGTTGGGCACTAAG	CTTAGTGCCCAACACCTGGATCGT

2006	CCAATCTAGGATACACCACGCCCG	CGGGCGTGGTGTATCCTAGATTGG
2007	GATACGTGGGGTATAGGCGGGCCC	GGGCCCGCCTATACCCCACGTATC
2008	CATGGAACAAACCGTCGTAGGGGA	TCCCCTACGACGGTTTGTTCCATG
2009	ACACTCGCGCAGTATTCGAGTCGT	ACGACTCGAATACTGCGCGAGTGT
2010	CTCAGTCTCGAAGGTGATCCGACC	GGTCGGATCACCTTCGAGACTGAG
2011	TCCCAATCCCCGTGGTATCGTCGT	ACGACGATACCACGGGGATTGGGA
2012	AATCAACGTAGTTCCGGTGGTCCG	CGGACCACCGGAACTACGTTGATT
2013	CTTAACAACCCAGGGGTTTGGGCT	AGCCCAAACCCCTGGGTTGTTAAG
2014	CTACCGCTGCATGGCGTTAGATTG	CAATCTAACGCCATGCAGCGGTAG
2015	TTATTGGTGGCGGACGGAGTGAGT	ACTCACTCCGTCCGCCACCAATAA
2016	TTAAGGGTGAACTCAACCGCGTGA	TCACGCGGTTGAGTTCACCCTTAA
2017	TTTGATTGAAACGCTGCGCACTAC	GTAGTGCGCAGCGTTTCAATCAAA
2018	TCATGTGTAGGTCGCGGCCGTCAC	GTGACGGCCGCGACCTACACATGA
2019	CTCCGAACCTTCTGGGCCTCTTTT	AAAAGAGGCCCAGAAGGTTCGGAG
2020	CTGTTGCCCATTGGCCCGACACTC	GAGTGTCGGGCCAATGGGCAACAG
2021	CACGATCGCTGAGCAACACATCAC	GTGATGTGTTGCTCAGCGATCGTG
2022	CGGATCATAAGCGTCCGCCTTCGT	ACGAAGGCGGACGCTTATGATCCG
2023	AGGTTAACGCAACATGTGATCCGC	GCGGATCACATGTTGCGTTAACCT
2024	GGGAAAAACAGCTAAGCCTTGCGA	TCGCAAGGCTTAGCTGTTTTTCCC
2025	ACTTATTGCCGGGATCCGTACACA	TGTGTACGGATCCCGGCAATAAGT
2026	TGCGGTCTGGAAAGGAAGGGAGGG	CCCTCCCTTCCTTTCCAGACCGCA
2027	GCTGCCACCTGGACATCGCATACA	TGTATGCGATGTCCAGGTGGCAGC
2028	GCAGGCATGACAGTGGCGTAGTAC	GTACTACGCCACTGTCATGCCTGC
2029	GCGGCCCTGATGGTTTGGCTGAGC	GCTCAGCCAAACCATCAGGGCCGC
2030	TCCCCATTTAGTCCCCTCCATCAC	GTGATGGAGGGGACTAAATGGGGA
2031	GCAACACAAATGCGAGCGTAGGAG	CTCCTACGCTCGCATTTGTGTTGC
2032	GGCGTTTGTATTCGAGCCACGTAG	CTACGTGGCTCGAATACAAACGCC
2033	GGTAACGTCGCACGTGGAATTCCG	CGGAATTCCACGTGCGACGTTACC
2034	ACTTCACAACGCTCCGTTGGACAC	GTGTCCAACGGAGCGTTGTGAAGT
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2036	GGACCCGATAAGACTCTGACGCCG	CGGCGTCAGAGTCTTATCGGGTCC
2037	ACCCGTTTCTCGTAGGAACCTGCT	AGCAGGTTCCTACGAGAAACGGGT
2038	CACGTTCGACTGTATCTGGTTGCC	GGCAACCAGATACAGTCGAACGTG
2039	CCTCGGATGGGCCCATGACCTTGA	TCAAGGTCATGGGCCCATCCGAGG
2040	GGACGCCTGCTGTAGGGGTTTGAT	ATCAAACCCCTACAGCAGGCGTCC
2041	CTCGAGCGTGGGCTAAAAGAGCAT	ATGCTCTTTTAGCCCACGCTCGAG
2042	TTTACTTCTTAGGGCGCGTTTGGG	CCCAAACGCGCCCTAAGAAGTAAA
2043	ACCACCAACATAGCGCGCACTAGT	ACTAGTGCGCGCTATGTTGGTGGT
2044	TGGTTACACGGCAGCCCGCGTAAG	CTTACGCGGGCTGCCGTGTAACCA
2045	TTATGGTACGTTGCTGCGTGCGGG	CCCGCACGCAGCAACGTACCATAA
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2047	CATGATCCCGCCCTTAGGTTAAGC	GCTTAACCTAAGGGCGGGATCATG
2048	TACCGCTTCAAAGGGTTGCCGAAT	ATTCGGCAACCCTTTGAAGCGGTA
2049	GCACCGCGTCAATATTACCGAGGA	TCCTCGGTAATATTGACGCGGTGC
2050	GTGTCGCGGCTTTACAGAAGGAGA	TCTCCTTCTGTAAAGCCGCGACAC
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2052	ATGAGGTCGTGCTGCGTTCACGAG	CTCGTGAACGCAGCACGACCTCAT
2053	CGAGACTAGTGCCGATGCAGGGTA	TACCCTGCATCGGCACTAGTCTCG
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2061	ACGAGTCCAACCGCCTCATTGATT	AATCAATGAGGCGGTTGGACTCGT
2062	GCGAAGAGTTGCTACTCTTCCGCC	GGCGGAAGAGTAGCAACTCTTCGC
2063	CGTCGGCAACAATCTTTTTCGTGA	TCACGAAAAAGATTGTTGCCGACG
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2068	AGTGCACCGGGTTGTGGACACAAT	ATTGTGTCCACAACCCGGTGCACT
2069	CCTGGCTTTTCACACGCCAAGAAA	TTTCTTGGCGTGTGAAAAGCCAGG
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2075	GTCCCATACGTGTGGTACGCGGAT	ATCCGCGTACCACACGTATGGGAC
2076	TCGGATACTCTCGCGTGCCACGGG	CCCGTGGCACGCGAGAGTATCCGA
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2078	GTTAGGTCACCGCGGCATATCCTA	TAGGATATGCCGCGGTGACCTAAC
2079	GTTCACCGGCCTCTACTTGGGTTT	AAACCCAAGTAGAGGCCGGTGAAC
2080	AATCCGCGTCTAGGTCATGTGGTC	GACCACATGACCTAGACGCGGATT
2081	GCTACGCCTCTGGAGGTGGTACCC	GGGTACCACCTCCAGAGGCGTAGC
2082	CAGGGAATGCTACAAAGGGTCCAA	TTGGACCCTTTGTAGCATTCCCTG
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2084	CCTCGCAAGCGCGATATTTATGCC	GGCATAAATATCGCGCTTGCGAGG
2085	GCCTCCCGGTCATGGTCAAGGGAA	TTCCCTTGACCATGACCGGGAGGC
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2091	CAGGAAGCTCGCTCCGTGATGCAC	GTGCATCACGGAGCGAGCTTCCTG
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2101	TGCTAACTGCGGCCCTACAGAGTC	GACTCTGTAGGGCCGCAGTTAGCA
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2126	TTACACGCTCGCTATTGGGCCATA	TATGGCCCAATAGCGAGCGTGTAA
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2130	AGTCCCTGCCGTTCGCTCATGGAA	TTCCATGAGCGAACGGCAGGGACT
2131	GGGCTTATGACCAGTCAGGTTGGA	TCCAACCTGACTGGTCATAAGCCC
2132	GGTCACCACACGAGTGCCTGGTCT	AGACCAGGCACTCGTGTGGTGACC
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2136	CAAATTCCTTGGGGGCCATAGTGG	CCACTATGGCCCCCAAGGAATTTG
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2142	TGGCGAGCAGACCTACAAGACAGA	TCTGTCTTGTAGGTCTGCTCGCCA
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2151	AAGCGACGATGCTTTCTTGAGCTG	CAGCTCAAGAAAGCATCGTCGCTT
2152	CACGGGCACGTGTTCTACGCTTGC	GCAAGCGTAGAACACGTGCCCGTG
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2155	ACTCTGGCTGTTGGCGAACGTGAC	GTCACGTTCGCCAACAGCCAGAGT
2156	GACCGAGGACCAGTCCTTGCTCTC	GAGAGCAAGGACTGGTCCTCGGTC
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2158	TTCTTGTCCTGGGGGAGAGCAGTG	CACTGCTCTCCCCCAGGACAAGAA
2159	TTAGCAGGGAGGTTGTCGGCTCAT	ATGAGCCGACAACCTCCCTGCTAA
2160	AGAACGTGGATTGTACGCTCCGCC	GGCGGAGCGTACAATCCACGTTCT
2161	CTTCACAGCCTGGAGCCACCAATG	CATTGGTGGCTCCAGGCTGTGAAG
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2163	GGGTCCAGAGTTGGTGTGGGATAA	TTATCCCACACCAACTCTGGACCC
2164	CCGTCCACCCCAGATAGGAATCAC	GTGATTCCTATCTGGGGTGGACGG
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2166	GATCACAGCGTCCGCGCATAACGG	CCGTTATGCGCGGACGCTGTGATC
2167	ATGACGCCTTACATGACGCACCTT	AAGGTGCGTCATGTAAGGCGTCAT
2168	GCGTGGAATAACGCCCTTAGTTCA	TGAACTAAGGGCGTTATTCCACGC
2169	GGTCTACCATTTCTCGCCCGACCG	CGGTCGGGCGAGAAATGGTAGACC

2170	ACACCTCTCTGGCGTAGACGCTCA	TGAGCGTCTACGCCAGAGAGGTGT
2171	GTAGAGGTGCTCAGGACTCGTCGC	GCGACGAGTCCTGAGCACCTCTAC
2172	GTAAGCAGGAGGCGAAGGCGCGAA	TTCGCGCCTTCGCCTCCTGCTTAC
2173	TCTAAGGGCCGTTTCAATCGACCT	AGGTCGATTGAAACGGCCCTTAGA
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2176	ACGATGCCGCGCATGTAACCTAGT	ACTAGGTTACATGCGCGGCATCGT
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2191	CGTTCATGCAAGGATCCCAGGTTA	TAACCTGGGATCCTTGCATGAACG
2192	ATGCCAATAGAAGCTGGGGATGCT	AGCATCCCCAGCTTCTATTGGCAT
2193	CCTAACTCTCCCTTGAGGCCGTTC	GAACGGCCTCAAGGGAGAGTTAGG
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2195	GCGACAGATTACGCTGCGGTTTTC	GAAAACCGCAGCGTAATCTGTCGC
2196	AAGCCCAGACGGCCAACACGTTAC	GTAACGTGTTGGCCGTCTGGGCTT
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2198	GATTGTCGTTCTGTCTGTGAGGCG	CGCCTCACAGACAGAACGACAATC
2199	ACCGAACTATGTTCCGGCATGGCA	TGCCATGCCGGAACATAGTTCGGT
2200	CGTCATCGGGTGTGCAATGCCGTT	AACGGCATTGCACACCCGATGACG
2201	CGGACGGAGTCACGTTTGTGCACT	AGTGCACAAACGTGACTCCGTCCG
2202	TAAACAAGTCGTGTGCCTTTGCCG	CGGCAAAGGCACACGACTTGTTTA
2203	TAATTACTGGCCTGTGGAGCAGGC	GCCTGCTCCACAGGCCAGTAATTA
2204	GGAGCGGCCCGAATGGTGCTCTTA	TAAGAGCACCATTCGGGCCGCTCC
2205	ACTAAGCAAGGCTTGGATGTGCGT	ACGCACATCCAAGCCTTGCTTAGT
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2207	GCGAGGCGAATTATCCGCGGATTT	AAATCCGCGGATAATTCGCCTCGC
2208	CATACGACACACCTTGGGGTGCTA	TAGCACCCCAAGGTGTGTCGTATG
2209	TGCTTGGGCTTTAAACCCCGTTTT	AAAACGGGGTTTAAAGCCCAAGCA
2210	CCGGTTGGAAAACGCAAATATCGG	CCGATATTTGCGTTTTCCAACCGG

2211	AAACTAGCTAGCCGCACCCGCAAG	CTTGCGGGTGCGGCTAGCTAGTTT
2212	GTTGTTCCACCAGTGATCACGCAG	CTGCGTGATCACTGGTGGAACAAC
2213	GCCGCTGACAAGATGATCATCGTT	AACGATGATCATCTTGTCAGCGGC
2214	CTTTCATAAAGCCAACCGATGCCC	GGGCATCGGTTGGCTTTATGAAAG
2215	CTGACTGCATCTCGAAAGCGGGTG	CACCCGCTTTCGAGATGCAGTCAG
2216	ATTTCTTCGGAGAATCGGCCACGT	ACGTGGCCGATTCTCCGAAGAAAT
2217	CATTTCGGGCCCTAGCTACTGCGC	GCGCAGTAGCTAGGGCCCGAAATG
2218	CCGATCCCGCACATCCGTATCCTG	CAGGATACGGATGTGCGGGATCGG
2219	TATCACCGGGAGCGTCTTATCGTG	CACGATAAGACGCTCCCGGTGATA
2220	TAGGGCTCGTGCACCGATTAGAGG	CCTCTAATCGGTGCACGAGCCCTA
2221	GCGTGGCACTCGCTTGTCTAGGTA	TACCTAGACAAGCGAGTGCCACGC
2222	CTCAACGAACTCAAGGGCCGCTAC	GTAGCGGCCCTTGAGTTCGTTGAG
2223	AGCCTGGTATCGACCAATCCTGCA	TGCAGGATTGGTCGATACCAGGCT
2224	TACGCGTTCTAGTTGGCCGGATCC	GGATCCGGCCAACTAGAACGCGTA
2225	TTTATGGGTTTGTGCCTGATGGGT	ACCCATCAGGCACAAACCCATAAA
2226	GGGACCCCTAGCAACGTCACCTTA	TAAGGTGACGTTGCTAGGGGTCCC
2227	CTGCCTCCCCAGGAGTCATTGGAT	ATCCAATGACTCCTGGGGAGGCAG
2228	AACCCCGCAAGACCAGTACCAATC	GATTGGTACTGGTCTTGCGGGGTT
2229	GGTCACATACGCGCTAAAAAGCGC	GCGCTTTTTAGCGCGTATGTGACC
2230	AAATGGCTCCGACCAGTTAGGGAC	GTCCCTAACTGGTCGGAGCCATTT
2231	AACGCGGCACGCTTAAAGGTGCAT	ATGCACCTTTAAGCGTGCCGCGTT
2232	GATCGCACGCCGATTAACCTTACA	TGTAAGGTTAATCGGCGTGCGATC
2233	CCTCCTGATTGGGAGTGCGGAATT	AATTCCGCACTCCCAATCAGGAGG
2234	CGGAGGGTAATAGGCTCCTCTGCG	CGCAGAGGAGCCTATTACCCTCCG
2235	ACAAGAACTGGACATTACCGCGGG	CCCGCGGTAATGTCCAGTTCTTGT
2236	TGTCGTCTTAAAGGCCTTTGTGCG	CGCACAAAGGCCTTTAAGACGACA
2237	GGTGACCATGTGGCGTTTTAGCTT	AAGCTAAAACGCCACATGGTCACC
2238	CACGGTTGCGCACGGTACCAGAAC	GTTCTGGTACCGTGCGCAACCGTG
2239	CCTTTATTGTTTGGTCCCCTGCCC	GGGCAGGGGACCAAACAATAAAGG
2240	GTGCGCCTGCATTCTACCGTCAAT	ATTGACGGTAGAATGCAGGCGCAC
2241	GTTTACGTTGATGGCTTGCCGCCG	CGGCGGCAAGCCATCAACGTAAAC
2242	CCGTCGGTGGTAGGACGTGAATGT	ACATTCACGTCCTACCACCGACGG
2243	TGATCGCCCCAGAATCCCTGTGCT	AGCACAGGGATTCTGGGGCGATCA
2244	AAGCAGCCAAAAATCGGTTGCTTT	AAAGCAACCGATTTTTGGCTGCTT
2245	CGACGGGACTTAGTAGCAGGGCCT	AGGCCCTGCTACTAAGTCCCGTCG
2246	CCGATTCGCGAAACGACCAAGTAG	CTACTTGGTCGTTTCGCGAATCGG
2247	CCACCCCAACTCCAATCTTTCTCA	TGAGAAAGATTGGAGTTGGGGTGG
2248	GTGCAGTAGACGACTACCGGCGTC	GACGCCGGTAGTCGTCTACTGCAC
2249	TTCGCCCATCGTATCAAGCAATTC	GAATTGCTTGATACGATGGGCGAA
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2251	CCAGCACTCGCCATCGGTTATAAT	ATTATAACCGATGGCGAGTGCTGG

2252	CGAACCGTAGAACTCCGGTCGGTG	CACCGACCGGAGTTCTACGGTTCG
2253	GCACCATGACAGAGCCCCAGGATG	CATCCTGGGGCTCTGTCATGGTGC
2254	TGGGCTACCGCAGAATAAGGGTGA	TCACCCTTATTCTGCGGTAGCCCA
2255	TGGCCTGTCGTGTCGAAGGAAACA	TGTTTCCTTCGACACGACAGGCCA
2256	GCCTCACCGATAGCGAGCGTTTGC	GCAAACGCTCGCTATCGGTGAGGC
2257	GTGCGCGCCGGCTAAAACGAGACA	TGTCTCGTTTTAGCCGGCGCGCAC
2258	CCGCAGACGAGTTTCTTGTGACAG	CTGTCACAAGAAACTCGTCTGCGG
2259	GTTCGCAATCGCGTGCTAGGAAGC	GCTTCCTAGCACGCGATTGCGAAC
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2261	CACTGAACACGATATAAGGGCGCG	CGCGCCCTTATATCGTGTTCAGTG
2262	CGCGATGGTTCTTAGCAAGACGAT	ATCGTCTTGCTAAGAACCATCGCG
2263	TACACCAAGGAAGAAATGGGGACG	CGTCCCCATTTCTTCCTTGGTGTA
2264	CGTGCCTTGCGTTTTAGGTGCAGC	GCTGCACCTAAAACGCAAGGCACG
2265	GTCGTTTGTCTGGGCATTAACGGC	GCCGTTAATGCCCAGACAAACGAC
2266	CAGGCTCTCGTTCGGTACAAACGT	ACGTTTGTACCGAACGAGAGCCTG
2267	CGGACACTGTTTCACCAGAACCCA	TGGGTTCTGGTGAAACAGTGTCCG
2268	TACCCATGATGCGGAAGAAGCGTA	TACGCTTCTTCCGCATCATGGGTA
2269	CTGTCCTTAAGCGGATGAGAACCG	CGGTTCTCATCCGCTTAAGGACAG
2270	CGGGAGATGAGAACGGTTTTGTGC	GCACAAAACCGTTCTCATCTCCCG
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2272	TAAAACAGTTCGCGCGACTGTCGT	ACGACAGTCGCGCGAACTGTTTTA
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2274	TGGCTAGGGATGGGGAATCATCTT	AAGATGATTCCCCATCCCTAGCCA
2275	AGGATTGGGTGCCTGGATGCATTG	CAATGCATCCAGGCACCCAATCCT
2276	TGTATCTACCGGCCTGAAGCAGGT	ACCTGCTTCAGGCCGGTAGATACA
2277	TCCCTACGCGCATGACTCGCTTAC	GTAAGCGAGTCATGCGCGTAGGGA
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2279	TGGGGGTAGTCCATGCATCAATTG	CAATTGATGCATGGACTACCCCCA
2280	CCCTGCCAGGATTACTATTCCGGA	TCCGGAATAGTAATCCTGGCAGGG
2281	TCCCGCACGGGGAATTTAAGTAGA	TCTACTTAAATTCCCCGTGCGGGA
2282	GTGATGTGCAGGAACTTCTGTCGC	GCGACAGAAGTTCCTGCACATCAC
2283	ATTTAGGCATGCATGCGCTTCTCA	TGAGAAGCGCATGCATGCCTAAAT
2284	TTCGGCGCTAGTGGACGCCGTCAA	TTGACGGCGTCCACTAGCGCCGAA
2285	GAGCTTCATCTCATCAGTTCCGCG	CGCGGAACTGATGAGATGAAGCTC
2286	GACAACTCCACTGCTCCAATCGCA	TGCGATTGGAGCAGTGGAGTTGTC
2287	GGCCAAGGATGGACCTTACGATGG	CCATCGTAAGGTCCATCCTTGGCC
2288	GGTTCCGGAATTTGTCACCGCTTC	GAAGCGGTGACAAATTCCGGAACC
2289	GCGCTGGATAGTCTGCGAGAAGCC	GGCTTCTCGCAGACTATCCAGCGC
2290	TGAGTCCAGTGCTGCCACCATGAA	TTCATGGTGGCAGCACTGGACTCA
2291	TTGAATTGGGTGTCGGAGCGTTCT	AGAACGCTCCGACACCCAATTCAA
2292	CGGCGGGCAGACAATGCTTTGAAC	GTTCAAAGCATTGTCTGCCCGCCG

2293	GGGTCTGTCAAAGAGGGTGTCTGG	CCAGACACCCTCTTTGACAGACCC
2294	CTTTGTGCAAGACGAAGCACCCTT	AAGGGTGCTTCGTCTTGCACAAAG
2295	ATCGAATTCCGAGGAGGTCTCCAT	ATGGAGACCTCCTCGGAATTCGAT
2296	TCCGACCCTCAGAGTCGACTCATT	AATGAGTCGACTCTGAGGGTCGGA
2297	ATCAACGGCCACCTCCTCGCCGAG	CTCGGCGAGGAGGTGGCCGTTGAT
2298	AGCCACGGAATAATTCCGTCCACC	GGTGGACGGAATTATTCCGTGGCT
2299	GATCGCTTGCGTATCGCAAAGACT	AGTCTTTGCGATACGCAAGCGATC
2300	TCCACGCCTTACCATCAACTGCAA	TTGCAGTTGATGGTAAGGCGTGGA
2301	GCCAAGCGATAGGCCAGAACTCAG	CTGAGTTCTGGCCTATCGCTTGGC
2302	AGCGTGTGGGTCATTTTAGCACGA	TCGTGCTAAAATGACCCACACGCT
2303	GTTATGCGCGGCTTACGAGTTCGA	TCGAACTCGTAAGCCGCGCATAAC
2304	TCTGTCCACGTAACTTGCCTGCAG	CTGCAGGCAAGTTACGTGGACAGA
2305	TCGGCAGCCAATGATCATACCTCT	AGAGGTATGATCATTGGCTGCCGA
2306	TAAGCCCGATCCGGTCCTGTGTTT	AAACACAGGACCGGATCGGGCTTA
2307	ACATGGCAGACTAACAGGCCTCGC	GCGAGGCCTGTTAGTCTGCCATGT
2308	CATGGCTGCACTCTAAGTCGAACG	CGTTCGACTTAGAGTGCAGCCATG
2309	TCTTCAACCCACGCGGAACGATTG	CAATCGTTCCGCGTGGGTTGAAGA
2310	CTCGTGTCTCCAGAGGATTGTCCC	GGGACAATCCTCTGGAGACACGAG
2311	TGAAGGCATCAACCCAGAGGATTT	AAATCCTCTGGGTTGATGCCTTCA
2312	ACAGCTCGAAGGCAGCCACATTGG	CCAATGTGGCTGCCTTCGAGCTGT
2313	ACAACGAGTACCGCGACAGAAGGG	CCCTTCTGTCGCGGTACTCGTTGT
2314	ATAACCGAAAAACCAGCCTGCGAT	ATCGCAGGCTGGTTTTTCGGTTAT
2315	ACAACTCAGCACTTTCGACGTCCA	TGGACGTCGAAAGTGCTGAGTTGT
2316	CGGGTTACTGGGTATCACCAATGC	GCATTGGTGATACCCAGTAACCCG
2317	CATCGGTTATCGCTGCACGCGCGT	ACGCGCGTGCAGCGATAACCGATG
2318	GAAGGAATCCCGGATAGTCCGTGG	CCACGGACTATCCGGGATTCCTTC
2319	GCATGGTCTCAGCCAAAGAACCTG	CAGGTTCTTTGGCTGAGACCATGC
2320	AGCCTGCGACGTTTCCCGACAGAC	GTCTGTCGGGAAACGTCGCAGGCT
2321	AAGAAAGGCGCACGGGATCGATAT	ATATCGATCCCGTGCGCCTTTCTT
2322	TGTCGCGAAGCCAACTTTCAGTAA	TTACTGAAAGTTGGCTTCGCGACA
2323	GCGGCATGCAAGGTAGGTCTGGAT	ATCCAGACCTACCTTGCATGCCGC
2324	GGTGGCCATCTCCTCGAATTGCAT	ATGCAATTCGAGGAGATGGCCACC
2325	GCGTGCATAAGTTGCACATTGTGC	GCACAATGTGCAACTTATGCACGC
2326	TTGAGGTAGCGTTTTCGCGCATAT	ATATGCGCGAAAACGCTACCTCAA
2327	ATCCCACTTGTGAGAGGGCGCATT	AATGCGCCCTCTCACAAGTGGGAT
2328	CGGTCAGCGAGCAGACATCAACCT	AGGTTGATGTCTGCTCGCTGACCG
2329	GCGTATCTTCGGGTCGAACACTTG	CAAGTGTTCGACCCGAAGATACGC
2330	ATGCCATTGAACTCGCACTTTGCG	CGCAAAGTGCGAGTTCAATGGCAT
2331	CGATTCCCATCATAATGTGGGTCC	GGACCCACATTATGATGGGAATCG
2332	CAATTTGGATAATCCAGCCACGCC	GGCGTGGCTGGATTATCCAAATTG
2333	CGGCTTACCCTATGATTCCGTGCA	TGCACGGAATCATAGGGTAAGCCG

2334	GGTGGACCATGCGCTGTGGTATGA	TCATACCACAGCGCATGGTCCACC
2335	TATTTGTCGAAGATCGCAAGCGCC	GGCGCTTGCGATCTTCGACAAATA
2336	GTCAGTGGGTTTTGAGAGCCCGCA	TGCGGGCTCTCAAAACCCACTGAC
2337	AGGGGGTCGGGAAATCTGACAAAA	TTTTGTCAGATTTCCCGACCCCCT
2338	TGCTTGCTATCCGAAAAAAGCAGG	CCTGCTTTTTTCGGATAGCAAGCA
2339	TTATCGGATCAAATTCGGCTTCGG	CCGAAGCCGAATTTGATCCGATAA
2340	TGCAGCAACGAGTTACCCGGACTT	AAGTCCGGGTAACTCGTTGCTGCA
2341	TATACATGTCCGGAGGGGCACCCA	TGGGTGCCCCTCCGGACATGTATA
2342	TGCAAAACCGGAGGATGAACCCTT	AAGGGTTCATCCTCCGGTTTTGCA
2343	TCGGTCTAATGTCCACGCAGACAC	GTGTCTGCGTGGACATTAGACCGA
2344	ATGTGTTTGCCACGCGCTCCTATT	AATAGGAGCGCGTGGCAAACACAT
2345	TGGCGAGGCACGGCTCTAATTCGG	CCGAATTAGAGCCGTGCCTCGCCA
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2347	CTCAGAGAGTCTATCCGGCGCCCT	AGGGCGCCGGATAGACTCTCTGAG
2348	GGAACATCTCCTGGGTCCCTCAGA	TCTGAGGGACCCAGGAGATGTTCC
2349	GCAACGCAGGGAAGTACTTAGCGA	TCGCTAAGTACTTCCCTGCGTTGC
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2352	CCCTTCTGACCGCTAAGGCCATAA	TTATGGCCTTAGCGGTCAGAAGGG
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2356	GAGTGACCTAATGGCTGCCCGACT	AGTCGGGCAGCCATTAGGTCACTC
2357	AAAGGAACTTGGCCAACCCTATGG	CCATAGGGTTGGCCAAGTTCCTTT
2358	TGTTTTCGCACTCCACCTAATCGC	GCGATTAGGTGGAGTGCGAAAACA
2359	CAATGGGTTTCATAAGGGCAGGCA	TGCCTGCCCTTATGAAACCCATTG
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2361	CGTCATGCGGTCCGAGGATCGATC	GATCGATCCTCGGACCGCATGACG
2362	CCACACGGGCACGGAGTAATATCT	AGATATTACTCCGTGCCCGTGTGG
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2365	GGCTACCCATAGGCTCAGCAGCAC	GTGCTGCTGAGCCTATGGGTAGCC
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2367	TGTGTTACGGCGAATGCAACAGTC	GACTGTTGCATTCGCCGTAACACA
2368	CGATAACAGGTCGCGCCGTTACTA	TAGTAACGGCGCGACCTGTTATCG
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2372	GGCATATCGGTAACACTTGGTCGG	CCGACCAAGTGTTACCGATATGCC
2373	GGGTCTCAAACCAGCGTGGCCGCT	AGCGGCCACGCTGGTTTGAGACCC
2374	GTCTCCGGGACCATTGAGCTGGAG	CTCCAGCTCAATGGTCCCGGAGAC

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2377	GGCAGGCCCGCGAGGATGATTAAC	GTTAATCATCCTCGCGGGCCTGCC
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2407	TGACGCCCATTTCTATATGGTGCA	TGCACCATATAGAAATGGGCGTCA
2408	TGTTCCGACAGGGCACTGCTAGAC	GTCTAGCAGTGCCCTGTCGGAACA
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2410	GTGCACCTCCGTTGGCGTAGAATG	CATTCTACGCCAACGGAGGTGCAC
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2414	ACCCGCGAACCGAGACGCACTTCT	AGAAGTGCGTCTCGGTTCGCGGGT
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2460	CCCATCTGGTGGGAGGCGTTATCA	TGATAACGCCTCCCACCAGATGGG
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2470	GATGCCTGGATCGGTCTAGCGTCA	TGACGCTAGACCGATCCAGGCATC
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2472	AGGGCTAATTTACATCGCCTTGCC	GGCAAGGCGATGTAAATTAGCCCT
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2476	TTGTCCAAAGCCACCTACGACAGA	TCTGTCGTAGGTGGCTTTGGACAA
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2492	AACCAAGACTCGTCCCCAAACGAA	TTCGTTTGGGGACGAGTCTTGGTT
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2499	TACCATACAAGAGAACGAGCCGCA	TGCGGCTCGTTCTCTTGTATGGTA
2500	GTAGCCGAGAGCAATTTTCACCGC	GCGGTGAAAATTGCTCTCGGCTAC
2501	GCAAACTCCCCTGCCCTTTAGCCT	AGGCTAAAGGGCAGGGGAGTTTGC
2502	ATCCCGCTGATAACCGCCAGGATA	TATCCTGGCGGTTATCAGCGGGAT
2503	AGTCTCAGTTCGGCGCAACGGTAG	CTACCGTTGCGCCGAACTGAGACT
2504	AACCTACAGTCGCCGCAATGCATT	AATGCATTGCGGCGACTGTAGGTT
2505	ATACACGTTTCAGCCGGCAACAAT	ATTGTTGCCGGCTGAAACGTGTAT
2506	ACGACGGGACGTGCCCTCGTTGAT	ATCAACGAGGGCACGTCCCGTCGT
2507	AAGTCCAAACTCGAATGGGGCAGT	ACTGCCCCATTCGAGTTTGGACTT
2508	GATTTATTGGCGCGGTAACGACCT	AGGTCGTTACCGCGCCAATAAATC
2509	TGTTTTCAGAGGCTACCCTGCCAT	ATGGCAGGGTAGCCTCTGAAAACA
2510	ACGGTCTCAGGGAAATGCGATCTC	GAGATCGCATTTCCCTGAGACCGT
2511	GACTTGAAACCGCCTATGCCCACA	TGTGGGCATAGGCGGTTTCAAGTC
2512	CGATCGGTTGTGTGCTGTCTTACC	GGTAAGACAGCACACAACCGATCG
2513	AGTAGCACAATGCCTCATTTCCGC	GCGGAAATGAGGCATTGTGCTACT
2514	CTCGCTATCTACGCGTCTCCGAAA	TTTCGGAGACGCGTAGATAGCGAG
2515	AGCCCGTTACGGCATCTAGGATTC	GAATCCTAGATGCCGTAACGGGCT
2516	TCGCGATGGCGAGAGTTCAGAATA	TATTCTGAACTCTCGCCATCGCGA
2517	TTACAGGATTCCAAAACCCGCAAA	TTTGCGGGTTTTGGAATCCTGTAA
2518	CGGTACCAACGCGCGGGCATATGA	TCATATGCCCGCGCGTTGGTACCG
2519	TGCCAGTATTATCCGTGCCAGCCG	CGGCTGGCACGGATAATACTGGCA
2520	ATTTCAGACCTCGGGACAACCTGG	CCAGGTTGTCCCGAGGTCTGAAAT
2521	GAAGTGCGCGTAACTTAGGGAGCC	GGCTCCCTAAGTTACGCGCACTTC
2522	TTGGCCAGGTCATCACTCTGCCAT	ATGGCAGAGTGATGACCTGGCCAA
2523	ATCGGCCGGTATTAGCTGCCCTCC	GGAGGGCAGCTAATACCGGCCGAT
2524	CGCAGGTAAGGCCGAGCAATGTTT	AAACATTGCTCGGCCTTACCTGCG
2525	TTGGGAACGTGCTAGGCGGCCCTC	GAGGGCCGCCTAGCACGTTCCCAA
2526	CATCTCGGCACACTGGTGCTGTAT	ATACAGCACCAGTGTGCCGAGATG
2527	ACGCGTAAATCAACGACGTGGTCG	CGACCACGTCGTTGATTTACGCGT
2528	CGTAGGTGGTAAATGTTGGCCCAG	CTGGGCCAACATTTACCACCTACG
2529	TTCGAGCCAGAATAAAACGGTTGG	CCAACCGTTTTATTCTGGCTCGAA
2530	AGAGATATTCGGCCTCGGTCGAGA	TCTCGACCGAGGCCGAATATCTCT
2531	CGACAAAGTTTCTCGCGAGCAACT	AGTTGCTCGCGAGAAACTTTGTCG
2532	ATTGCCGCGTCTCGTATCAAAAGA	TCTTTTGATACGAGACGCGGCAAT
2533	CGGAGAATGGATGCAGGTTCTTCG	CGAAGAACCTGCATCCATTCTCCG
2534	TATAATCATTTGCGACTCGCCCCA	TGGGGCGAGTCGCAAATGATTATA
2535	AATTTTCCCCGATTTGAAGAAGCG	CGCTTCTTCAAATCGGGGAAAATT
2536	TCGCATACTTCGTCGGCGAGTATT	AATACTCGCCGACGAAGTATGCGA
2537	CGTGAGCCGTTCTCATCCAAGCGG	CCGCTTGGATGAGAACGGCTCACG
2538	GCAGAATCGAATTGGGGTGGGTTT	AAACCCACCCCAATTCGATTCTGC

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2540	GACCAGTTAGTGCAATGGTTGGCG	CGCCAACCATTGCACTAACTGGTC
2541	TTCTCGCACAGCTAGTCAGCCGAT	ATCGGCTGACTAGCTGTGCGAGAA
2542	CCAAGTCTTGCGTGAGCGATCCTG	CAGGATCGCTCACGCAAGACTTGG
2543	GCGAAAGTGGCTCGTATTTCTCCA	TGGAGAAATACGAGCCACTTTCGC
2544	CCTCGGGACTGTCCGACTGAAAAA	TTTTTCAGTCGGACAGTCCCGAGG
2545	AGGCGAGTGTACGGCTCATCCATG	CATGGATGAGCCGTACACTCGCCT
2546	GCGGCTCTGCCTACGATATTCACA	TGTGAATATCGTAGGCAGAGCCGC
2547	TGCACCTGTCTGTAGATTTGCGGT	ACCGCAAATCTACAGACAGGTGCA
2548	CATAAAGCACGGACGCGACTTGAT	ATCAAGTCGCGTCCGTGCTTTATG
2549	CCCTCAACGTAGGGCGTGACTTTC	GAAAGTCACGCCCTACGTTGAGGG
2550	GGGTCATCGTGCAGTTATGCCGTA	TACGGCATAACTGCACGATGACCC
2551	CCCGGATAATCCTTTGTCCAGCCG	CGGCTGGACAAAGGATTATCCGGG
2552	TCCGATAAGCGAACTCACATGGGT	ACCCATGTGAGTTCGCTTATCGGA
2553	CCTGCTGGTTCGGTCGTAAGCGAA	TTCGCTTACGACCGAACCAGCAGG
2554	GAGGCACCAATCGGTCTGAAAATG	CATTTTCAGACCGATTGGTGCCTC
2555	TACGAAAATGGTTGCGCCGGGTCT	AGACCCGGCGCAACCATTTTCGTA
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2557	CCGAATCAGCCGTATTTGCTGGAA	TTCCAGCAAATACGGCTGATTCGG
2558	CCCGCTTATCTGTACTCGATCGCA	TGCGATCGAGTACAGATAAGCGGG
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2560	AGTGACAGCGCTCACCACGGTCCC	GGGACCGTGGTGAGCGCTGTCACT
2561	CCATGAGTGTTTCGGGACATCGTA	TACGATGTCCCGAAACACTCATGG
2562	GCCACATTCTGCTACCTCCGTGTT	AACACGGAGGTAGCAGAATGTGGC
2563	TCCTGTGCTTTGTGACGTGCTAGG	CCTAGCACGTCACAAAGCACAGGA
2564	GACCGCATATACACCTGATGGGCC	GGCCCATCAGGTGTATATGCGGTC
2565	GTAGGCCCGTCGTTAACCATCTCA	TGAGATGGTTAACGACGGGCCTAC
2566	CGGCTCGCGAAATGGAGTTTAGCG	CGCTAAACTCCATTTCGCGAGCCG
2567	GCTGATCGGCTTTTCACCGCTATA	TATAGCGGTGAAAAGCCGATCAGC
2568	TATCAAATCGTTGGCACGCGACTA	TAGTCGCGTGCCAACGATTTGATA
2569	TTGGCGAGGATCCCTAGGCGTACT	AGTACGCCTAGGGATCCTCGCCAA
2570	AAGTCCTGAGGCCGTTCGGTTTCT	AGAAACCGAACGGCCTCAGGACTT
2571	ACTCCGGACATCTCGGCCAGAGAT	ATCTCTGGCCGAGATGTCCGGAGT
2572	CCAAGGGGAACACAGGATCGTAGA	TCTACGATCCTGTGTTCCCCTTGG
2573	GTGGCCTAAATCCGCCTTCTCAAC	GTTGAGAAGGCGGATTTAGGCCAC
2574	CACTCCGTCTCGTCCATTAATGCG	CGCATTAATGGACGAGACGGAGTG
2575	TCAAGAACCCAGTGCCGGTCAGCA	TGCTGACCGGCACTGGGTTCTTGA
2576	GAATCAATTTTCCAGGGACGGGAC	GTCCCGTCCCTGGAAAATTGATTC
2577	ATCGGTGTGCTGGAGCGCCAGAGT	ACTCTGGCGCTCCAGCACACCGAT
2578	GCCTCTCCTATGACGATGACCCAC	GTGGGTCATCGTCATAGGAGAGGC
2579	TGGGCGCGCTTTTAAGACTACATC	GATGTAGTCTTAAAAGCGCGCCCA

2580	CGTTGGGTACCGTTCTATCAACCG	CGGTTGATAGAACGGTACCCAACG
2581	GCAGTGAGCTGGGTTCAATGCTTC	GAAGCATTGAACCCAGCTCACTGC
2582	CATCATCCACACAGGCAGGTGTGT	ACACACCTGCCTGTGTGGATGATG
2583	AGACAAAGGTCCCCATTGCGAAAT	ATTTCGCAATGGGGACCTTTGTCT
2584	ATACTCGTCGACGAGAAGCGGAAA	TTTCCGCTTCTCGTCGACGAGTAT
2585	GCAGAATGTGTTGTCTTCGCAGCC	GGCTGCGAAGACAACACATTCTGC
2586	CACCATGCCTTCATCTTGGCCTAG	CTAGGCCAAGATGAAGGCATGGTG
2587	ACTCTTCAACGCCAGGTTAAGCCA	TGGCTTAACCTGGCGTTGAAGAGT
2588	GCGACCTGCGGCGTGTGTATTCTC	GAGAATACACACGCCGCAGGTCGC
2589	TCGGTGTATGCACCCTTTCTCCAT	ATGGAGAAAGGGTGCATACACCGA
2590	ACCGTCGAATCTTGCGGCCAATGT	ACATTGGCCGCAAGATTCGACGGT
2591	TAATGCATGCTCCCGGCTCACGTT	AACGTGAGCCGGGAGCATGCATTA
2592	TCTGTACACACCACGTCGTGCACA	TGTGCACGACGTGGTGTGTACAGA
2593	CATGGGGTTGTCAGACGACACCTA	TAGGTGTCGTCTGACAACCCCATG
2594	AATCTGATGCTCGCTGTAGGACGG	CCGTCCTACAGCGAGCATCAGATT
2595	TCGAAACCGCGGGAAAGGGTAAAA	TTTTACCCTTTCCCGCGGTTTCGA
2596	TGGGGGACGGGCGTCTAATCCTCC	GGAGGATTAGACGCCCGTCCCCCA
2597	AGGCATGCACCCATGCTGCCAGAG	CTCTGGCAGCATGGGTGCATGCCT
2598	TCCCAATGGCCTGTCAAGCATAAA	TTTATGCTTGACAGGCCATTGGGA
2599	GAACCTGAGCCTTTGCTAGCACGA	TCGTGCTAGCAAAGGCTCAGGTTC
2600	CGAATTGATAGCGTTACGGGCGAA	TTCGCCCGTAACGCTATCAATTCG
2601	TTGCACGCGCGCGAACGACTATTC	GAATAGTCGTTCGCGCGCGTGCAA
2602	TGCGGTGAAGCAGTCCAAGGTCAG	CTGACCTTGGACTGCTTCACCGCA
2603	TGAGGACCATCCAATGGATCGGTT	AACCGATCCATTGGATGGTCCTCA
2604	TCGGTGATTGGTAATTTGGATCCG	CGGATCCAAATTACCAATCACCGA
2605	GCGGGCAGGTAGTTTGACTGGATG	CATCCAGTCAAACTACCTGCCCGC
2606	CAAGCACAAGCCCATGAAATTTCA	TGAAATTTCATGGGCTTGTGCTTG
2607	CGGTACAGCGGATAGCCAAGGATA	TATCCTTGGCTATCCGCTGTACCG
2608	CCATGCTCTTCGCTGCAGCATACT	AGTATGCTGCAGCGAAGAGCATGG
2609	CGCGGCAAAGATTAATTCCCGGCG	CGCCGGGAATTAATCTTTGCCGCG
2610	GAAGACCCGTCCGGGTTTCCATAC	GTATGGAAACCCGGACGGGTCTTC
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2621	CCATAGACTAGCGCCAGAGTGCCC	GGGCACTCTGGCGCTAGTCTATGG
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2623	GAATAATCATCGCGGTCCTCATGG	CCATGAGGACCGCGATGATTATTC
2624	GGGATTGGCTCTTGGTTGGAAGAA	TTCTTCCAACCAAGAGCCAATCCC
2625	ATTGTGCTTCCTCGAACTGGGAAA	TTTCCCAGTTCGAGGAAGCACAAT
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2627	TCAGGACCGACGGTGCACTTAGTG	CACTAAGTGCACCGTCGGTCCTGA
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2633	TGCAGGCTTCTCAACGGCTGGGAG	CTCCCAGCCGTTGAGAAGCCTGCA
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2636	CGAACCGGCAGTCGATCGTTGCAT	ATGCAACGATCGACTGCCGGTTCG
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2643	ATGGTTCAGAAGGTTCGTCGGGTT	AACCCGACGAACCTTCTGAACCAT
2644	GAGTGGAGCATTCTCGGCCCTCAA	TTGAGGGCCGAGAATGCTCCACTC
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2646	TGCTCTTGTGGTCACTCGAGAGGA	TCCTCTCGAGTGACCACAAGAGCA
2647	TTGGGAGCACGGTTACCGCCTGTG	CACAGGCGGTAACCGTGCTCCCAA
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2781	GAAAATCACGGTAAGGCACGTTCG	CGAACGTGCCTTACCGTGATTTTC
2782	GATTCTCGCTTCCCAACGAGCATA	TATGCTCGTTGGGAAGCGAGAATC
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2784	CGATCCTGCGTGCCTCATCCAGGC	GCCTGGATGAGGCACGCAGGATCG

2785	CCCTCAAGTGGGCGAGGGTTTTCA	TGAAAACCCTCGCCCACTTGAGGG
2786	TCGCCTCCGCCTCGTGTGTAGAAG	CTTCTACACACGAGGCGGAGGCGA
2787	TTCGCTTTCAGCTCATTGGAACGA	TCGTTCCAATGAGCTGAAAGCGAA
2788	TGTAATCTGAACAAGCGGACCCCT	AGGGGTCCGCTTGTTCAGATTACA
2789	TGGAATCTTTCTTGAGCGCCGTGA	TCACGGCGCTCAAGAAAGATTCCA
2790	GGCTTTCATCTTTAACCGCTCGGT	ACCGAGCGGTTAAAGATGAAAGCC
2791	TGATCCGAGCCATTCCTAATCACC	GGTGATTAGGAATGGCTCGGATCA
2792	TGGTAGGCGTGATGTCCTACGCAA	TTGCGTAGGACATCACGCCTACCA
2793	AGGCATCGGTAAGAAGGCCCTATG	CATAGGGCCTTCTTACCGATGCCT
2794	CGCCGCGAGACGATCCTTATTATT	AATAATAAGGATCGTCTCGCGGCG
2795	ACATGGACGAAATTACGCCCGTCA	TGACGGGCGTAATTTCGTCCATGT
2796	ACAGAAAGGTGGGGAGCCTAGCGT	ACGCTAGGCTCCCCACCTTTCTGT
2797	AGGCTTGCGAACATGGGTAGTGAC	GTCACTACCCATGTTCGCAAGCCT
2798	GCGTGGGCCTTGCTCCTGTTTAAC	GTTAAACAGGAGCAAGGCCCACGC
2799	GAATACAGAGCGTCCGATGTGCCC	GGGCACATCGGACGCTCTGTATTC
2800	GCGACTCTGTAGGGAGCGCGATAT	ATATCGCGCTCCCTACAGAGTCGC
2801	GGTGCACTCATATGCGTCGCATCG	CGATGCGACGCATATGAGTGCACC
2802	CTGTCCCACGGGGAAACCTTACTT	AAGTAAGGTTTCCCCGTGGGACAG
2803	TGGCTTACTGTCGCAATCTAGGCC	GGCCTAGATTGCGACAGTAAGCCA
2804	GCACTCAGTTTCCGGTATCCCATG	CATGGGATACCGGAAACTGAGTGC
2805	GTGAGGTTCACGTAAGGCACAGCG	CGCTGTGCCTTACGTGAACCTCAC
2806	GTAACGCCTTTGTCCCCAGCGTAT	ATACGCTGGGGACAAAGGCGTTAC
2807	GCATTGATATGGTCGGTCTCGCCT	AGGCGAGACCGACCATATCAATGC
2808	GTGGGTTTAAGTGACAACGGACGC	GCGTCCGTTGTCACTTAAACCCAC
2809	CAAAACCCTGCCGAAGATGTTGGT	ACCAACATCTTCGGCAGGGTTTTG
2810	TCCGAGGAGACTGAACCTGCTACC	GGTAGCAGGTTCAGTCTCCTCGGA
2811	CGGGGAAGAACGGATTCGCTAAAT	ATTTAGCGAATCCGTTCTTCCCCG
2812	TGGTTAGCTTATGTCGGAGCCACC	GGTGGCTCCGACATAAGCTAACCA
2813	ACGCGTCGATGAACTAAGGCTCGC	GCGAGCCTTAGTTCATCGACGCGT
2814	TTCTCCTGACGAGTACGCAGTGGG	CCCACTGCGTACTCGTCAGGAGAA
2815	TCCGCGGTTGCCGGTTTGTTAGGA	TCCTAACAAACCGGCAACCGCGGA
2816	TGGCGCATCTTTCAGGGGATGATG	CATCATCCCCTGAAAGATGCGCCA
2817	TCTTTGGTCCTTGGTGTTTACGCG	CGCGTAAACACCAAGGACCAAAGA
2818	GAGAACTCCCGCTACAAAGGAGCC	GGCTCCTTTGTAGCGGGAGTTCTC
2819	TTAACGTGGGAACCGTTGGTGAAT	ATTCACCAACGGTTCCCACGTTAA
2820	GGGACACCATCCTTGGGTTTGTTA	TAACAAACCCAAGGATGGTGTCCC
2821	CAACAAACCGCCTTGGGAAGTGAC	GTCACTTCCCAAGGCGGTTTGTTG
2822	TTGAAGGCCACCGATACTGATCGC	GCGATCAGTATCGGTGGCCTTCAA
2823	TCGTAATAGAACTGCGCCCAATGC	GCATTGGGCGCAGTTCTATTACGA
2824	GGCACGTTGCCCAAGTTGGATCCA	TGGATCCAACTTGGGCAACGTGCC
2825	ACATAGCTTGGCCGGACACCCACC	GGTGGGTGTCCGGCCAAGCTATGT

2826	CTTGCCGCCTTGCGAGTGGCTAAA	TTTAGCCACTCGCAAGGCGGCAAG
2827	AATGGCTCGCCAGATACCGCAGCC	GGCTGCGGTATCTGGCGAGCCATT
2828	CAAAAGGCGTGTCCGAACTTTTCA	TGAAAAGTTCGGACACGCCTTTTG
2829	CGTCCACTTAGGTGGAGATACGCC	GGCGTATCTCCACCTAAGTGGACG
2830	GAGCCTCTTCGTCCTGAAGACCGA	TCGGTCTTCAGGACGAAGAGGCTC
2831	AACATCAAGCGGCAATCTCCCTTC	GAAGGGAGATTGCCGCTTGATGTT
2832	CGTCCTGACATTATTAGCGCGTGC	GCACGCGCTAATAATGTCAGGACG
2833	TGTGCAGACCCTAACGACCTACGG	CCGTAGGTCGTTAGGGTCTGCACA
2834	TTAGGTCGGCCTAGACCCTCCGTA	TACGGAGGGTCTAGGCCGACCTAA
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2836	AGACCTTCCCACGCGAGATGCTAC	GTAGCATCTCGCGTGGGAAGGTCT
2837	TTCTTGCCAAAATGTGTCCAACCA	TGGTTGGACACATTTTGGCAAGAA
2838	CAGTTTTCATTGCAGCGAAAGCAA	TTGCTTTCGCTGCAATGAAAACTG
2839	GTGCCGATCCCGAGACAAGTTCCG	CGGAACTTGTCTCGGGATCGGCAC
2840	CATCCGGCCTCAGTGATTCTTACC	GGTAAGAATCACTGAGGCCGGATG
2841	TGCTGGAAGCCACAAACGTTACGT	ACGTAACGTTTGTGGCTTCCAGCA
2842	GAACGGCCAGGGGACAACTATCGT	ACGATAGTTGTCCCCTGGCCGTTC
2843	TCATCTAGGTCGAAGCGCAAGACA	TGTCTTGCGCTTCGACCTAGATGA
2844	TTTGGTTACCAGCACCCATGTTCC	GGAACATGGGTGCTGGTAACCAAA
2845	GACAACAGTCTGTCCGCCACATCC	GGATGTGGCGGACAGACTGTTGTC
2846	GCCAACAGGAGATGCTTGCACCAT	ATGGTGCAAGCATCTCCTGTTGGC
2847	CTAAGGACGCATTGACCCCTGAAC	GTTCAGGGGTCAATGCGTCCTTAG
2848	GGTCGCGTAGTGAGTCAGAGGCGT	ACGCCTCTGACTCACTACGCGACC
2849	TTACCTCATGAACCCTTCGCGGCG	CGCCGCGAAGGGTTCATGAGGTAA
2850	TATACAGCATCGTCGCCGGGCATA	TATGCCCGGCGACGATGCTGTATA
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2852	TGCACTCCGCAACCTTGTGAAATC	GATTTCACAAGGTTGCGGAGTGCA
2853	AACCCGTCATGCCGACTCCATCTA	TAGATGGAGTCGGCATGACGGGTT
2854	AGCACTAGTGGCGTGCGACTTTGC	GCAAAGTCGCACGCCACTAGTGCT
2855	TAAAAAGTGCCGCTAACCACGGAG	CTCCGTGGTTAGCGGCACTTTTTA
2856	CGCGGAATATTTGTCGTCCGATTC	GAATCGGACGACAAATATTCCGCG
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2858	CGAACTACTGCGTCAGCCTCTCCC	GGGAGAGGCTGACGCAGTAGTTCG
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2860	AATAACAGTGGCAATGAGCGGGAA	TTCCCGCTCATTGCCACTGTTATT
2861	ATATGTTGATTCCCGTGCTGCACA	TGTGCAGCACGGGAATCAACATAT
2862	AGAGTGGGCACCACCAGGCAGACA	TGTCTGCCTGGTGGTGCCCACTCT
2863	AGGCCTGGGTTTCTGCGTCTTAGT	ACTAAGACGCAGAAACCCAGGCCT
2864	CGGACGTGACAAACGGACATACCC	GGGTATGTCCGTTTGTCACGTCCG
2865	CAAGTGTTTCGGCCCAACTCTCGA	TCGAGAGTTGGGCCGAAACACTTG
2866	GAACCCTTATCGGGATAGGCCCAA	TTGGGCCTATCCCGATAAGGGTTC

2867	CAGGACGATACCAAGCAGAACGCC	GGCGTTCTGCTTGGTATCGTCCTG
2868	GCGTCTTGTGATTCTGCCCTAACC	GGTTAGGGCAGAATCACAAGACGC
2869	AAACAACCATCAATGTCGGGTCCA	TGGACCCGACATTGATGGTTGTTT
2870	TGTAAAGACCAGTTGGCGGCTCTC	GAGAGCCGCCAACTGGTCTTTACA
2871	GCGTTTTGACTCGGTGGTCAGTCC	GGACTGACCACCGAGTCAAAACGC
2872	TGTATGGAGGCACGGCAAAGTCTT	AAGACTTTGCCGTGCCTCCATACA
2873	TTACCTAGGTTCCCGCTGACACGC	GCGTGTCAGCGGGAACCTAGGTAA
2874	CGGCTCGTGGGAATCCTCTGAAGA	TCTTCAGAGGATTCCCACGAGCCG
2875	CCGGCTCGGGCATTTCTTGGACCT	AGGTCCAAGAAATGCCCGAGCCGG
2876	CAACGATGGAATTGTCTCCTTGGG	CCCAAGGAGACAATTCCATCGTTG
2877	CGGGCTATTATCGGGATTATGGGG	CCCCATAATCCCGATAATAGCCCG
2878	ACGTACCTGAAGATGCAACGGCGG	CCGCCGTTGCATCTTCAGGTACGT
2879	CATGGTGCAGCACGCACAAGTAAC	GTTACTTGTGCGTGCTGCACCATG
2880	CGTCGATATGTCGGGCTATTGCCT	AGGCAATAGCCCGACATATCGACG
2881	AAATGCAGGGTTAAGAGGAGGCCC	GGGCCTCCTCTTAACCCTGCATTT
2882	TGCAAGGACTGATTCTCCCGCTGT	ACAGCGGGAGAATCAGTCCTTGCA
2883	GTTTTCGGAACGCCGCAGAGTTCA	TGAACTCTGCGGCGTTCCGAAAAC
2884	CCCTCGATGGTTCATTGGGAAGAC	GTCTTCCCAATGAACCATCGAGGG
2885	CCTGTTCGCTCATAATGGTGGGGT	ACCCCACCATTATGAGCGAACAGG
2886	GAAAGAACGATCGCGGAATAGCTG	CAGCTATTCCGCGATCGTTCTTTC
2887	TCCACCTGTGTGCCTTTATCCTCA	TGAGGATAAAGGCACACAGGTGGA
2888	TCCTCCGTGAACCGCTGTAGCGCA	TGCGCTACAGCGGTTCACGGAGGA
2889	TTGAGATTTTTACGGTTTCCCCGC	GCGGGGAAACCGTAAAAATCTCAA
2890	CGATAGGACGTGGGCATGTCCCAG	CTGGGACATGCCCACGTCCTATCG
2891	CCCGAACTTTGAGATCCGAGAACA	TGTTCTCGGATCTCAAAGTTCGGG
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2893	AGATAACGCCCACTGACGACATGC	GCATGTCGTCAGTGGGCGTTATCT
2894	ACGCTTAGAGCTCCGATGCCGAAT	ATTCGGCATCGGAGCTCTAAGCGT
2895	GGGCGATAACTTAAATTGTGCCGC	GCGGCACAATTTAAGTTATCGCCC
2896	AGGACGTTCATGCGTCTCTTTGCA	TGCAAAGAGACGCATGAACGTCCT
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2899	GCAGGTTGGCTGTCTTGTGGAGTC	GACTCCACAAGACAGCCAACCTGC
2900	CGTTTGGTTGCTTCAAGAACCGGT	ACCGGTTCTTGAAGCAACCAAACG
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2902	GGGGTCGGCTGAAGTGTTTTATCC	GGATAAAACACTTCAGCCGACCCC
2903	GTGACGGTTGATTAACGACCGTGG	CCACGGTCGTTAATCAACCGTCAC
2904	CTTATGGCAGCGCCAGGGGCACTC	GAGTGCCCCTGGCGCTGCCATAAG
2905	GTTAGGGGACCCACCTCGTTTGAT	ATCAAACGAGGTGGGTCCCCTAAC
2906	CAATATAAATGCCGCGCATCGAGT	ACTCGATGCGCGGCATTTATATTG
2907	TTCTTCATCAGCAGTCCCCGAGAA	TTCTCGGGGACTGCTGATGAAGAA

2908	AGTTGCGTCCCTTGATGGCATTTT	AAAATGCCATCAAGGGACGCAACT
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2910	ACTTGGCCGGACGACAGCAAAGAC	GTCTTTGCTGTCGTCCGGCCAAGT
2911	CACCGCGGTAGATGTATCCCTTCC	GGAAGGGATACATCTACCGCGGTG
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2913	GCGCATAAGAAGGTCCGCTAAAGC	GCTTTAGCGGACCTTCTTATGCGC
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2922	GTATACCGGTGCATGCTGAAGCAA	TTGCTTCAGCATGCACCGGTATAC
2923	AGTGTTCTGGTTCGAGTCGACCCG	CGGGTCGACTCGAACCAGAACACT
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2931	TGTGCGTGCTTATGTTCCGGTCTC	GAGACCGGAACATAAGCACGCACA
2932	CAACCGTTGGCCGTAACAAAAATC	GATTTTTGTTACGGCCAACGGTTG
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2935	GATGGTGTTTTCGCCAAGACCAAT	ATTGGTCTTGGCGAAAACACCATC
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2940	CAGGCGTAAACCTGAACCAAACGG	CCGTTTGGTTCAGGTTTACGCCTG
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2946	TTTTACCTGGCCATTGGTGAGCTC	GAGCTCACCAATGGCCAGGTAAAA
2947	CTCTACTCAATCAGGGTGGGAGCG	CGCTCCCACCCTGATTGAGTAGAG
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2992	GGCTCCGAATCTCTTGTCCGGTCT	AGACCGGACAAGAGATTCGGAGCC
2993	AGGATGGCCACGCCGAATCAAAGT	ACTTTGATTCGGCGTGGCCATCCT
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2996	ACTCCGCTTCAATGGAGACCGTTG	CAACGGTCTCCATTGAAGCGGAGT
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3069	GGCACCCAATACCACGAAGAAGAA	TTCTTCTTCGTGGTATTGGGTGCC
3070	AGGGGCATTTCGAACTCCATCTTT	AAAGATGGAGTTCGAAATGCCCCT
3071	CATCATCACAAAGGAACGTCGGTG	CACCGACGTTCCTTTGTGATGATG

3072	TAAAGACCCACCGTCAGCAGCAGC	GCTGCTGCTGACGGTGGGTCTTTA
3073	CCCCAGGCGTAATGCACCACATAG	CTATGTGGTGCATTACGCCTGGGG
3074	GCAGGTCGAACGCTAGTGGTTGAA	TTCAACCACTAGCGTTCGACCTGC
3075	GGAACTTAGGAGTTCACGTCGCCA	TGGCGACGTGAACTCCTAAGTTCC
3076	GCAGATACGGCTAGCTGAGGTGGC	GCCACCTCAGCTAGCCGTATCTGC
3077	CACAGGCCTAGAGCCTCGGCGTTC	GAACGCCGAGGCTCTAGGCCTGTG
3078	GTTTTGCGCGCATGAGGTTCATTA	TAATGAACCTCATGCGCGCAAAAC
3079	TTGCGCCTGATGCCAGCAGTACTA	TAGTACTGCTGGCATCAGGCGCAA
3080	GATATCAGGCTTTCCCACTGCCGC	GCGGCAGTGGGAAAGCCTGATATC
3081	TGCGCGGAGACGGAGATCTATGAA	TTCATAGATCTCCGTCTCCGCGCA
3082	CATTGGTGTTGGCTGAGAGTGGAC	GTCCACTCTCAGCCAACACCAATG
3083	GTCGGCACTTGGGCACCATTAATA	TATTAATGGTGCCCAAGTGCCGAC
3084	ATCGATCGGTGTCTCACCACGGAG	CTCCGTGGTGAGACACCGATCGAT
3085	CGTAGCCTTCCACCGTGTCGATAG	CTATCGACACGGTGGAAGGCTACG
3086	CGCTCTCCGTCTGAGGAAAAGGGG	CCCCTTTTCCTCAGACGGAGAGCG
3087	TCGCCCCAGCCAAGGATATATTGC	GCAATATATCCTTGGCTGGGGCGA
3088	TCTCTTGCAAGGAACTCTGCCGTC	GACGGCAGAGTTCCTTGCAAGAGA
3089	GTCCTGGACAGACGGAGGGTGTTA	TAACACCCTCCGTCTGTCCAGGAC
3090	GCCAAATTAAGCGGGCTCGTAATC	GATTACGAGCCCGCTTAATTTGGC
3091	CCATTTGTTGACCGATGGGAGGGG	CCCCTCCCATCGGTCAACAAATGG
3092	TGGTCAAAAGAGCACGATCCAGGA	TCCTGGATCGTGCTCTTTTGACCA
3093	CGCTACTAAGACGCCCCTGTCCAC	GTGGACAGGGGCGTCTTAGTAGCG
3094	CATACCTCCCGCTTGGATTCACTG	CAGTGAATCCAAGCGGGAGGTATG
3095	CCGCGGAAGGAATGTCATCTACAA	TTGTAGATGACATTCCTTCCGCGG
3096	CACGGGACATTCATTCACAGGACG	CGTCCTGTGAATGAATGTCCCGTG
3097	AGGAGTCACCCACTCCGCACAAAA	TTTTGTGCGGAGTGGGTGACTCCT
3098	TCATGACAGCGCACCCCATACCAT	ATGGTATGGGGTGCGCTGTCATGA
3099	GGTAGGGGACTATCGATCGTGCTG	CAGCACGATCGATAGTCCCCTACC
3100	ATGTCTCACTACCGCACGTAGCGG	CCGCTACGTGCGGTAGTGAGACAT
3101	ACGGAGGAGCGACTCGTTCGCTGC	GCAGCGAACGAGTCGCTCCTCCGT
3102	GAAGTCTGTCGCCGGTGGACGGAC	GTCCGTCCACCGGCGACAGACTTC
3103	CCGTAACGTGTATTCGGACGAGCG	CGCTCGTCCGAATACACGTTACGG
3104	CGTGGAAGCGACTTAACCAATCGT	ACGATTGGTTAAGTCGCTTCCACG
3105	GGCATGGGCTATGCCTCACACTAG	CTAGTGTGAGGCATAGCCCATGCC
3106	GGGTCGTATTTCAGCATCGTTCGT	ACGAACGATGCTGAAATACGACCC
3107	AATGGTCGCGCAAACCGTAAGAAT	ATTCTTACGGTTTGCGCGACCATT
3108	CTGGATTCGGTACGTCCAACGTTT	AAACGTTGGACGTACCGAATCCAG
3109	CGCAAAAACACCCGTAGCCAAGAA	TTCTTGGCTACGGGTGTTTTTGCG
3110	TATGGATACGCTTTTGGACTGGGC	GCCCAGTCCAAAAGCGTATCCATA
3111	GCTTCAAACGCGCTTCACGCTGGT	ACCAGCGTGAAGCGCGTTTGAAGC
3112	TACAGCCCGCTCTACCTCGCCACC	GGTGGCGAGGTAGAGCGGGCTGTA

3113	TCAACCGATGTCAAAATGCACGTT	AACGTGCATTTTGACATCGGTTGA
3114	AGCTCTCTCCGAAGTAGGGCGGTA	TACCGCCCTACTTCGGAGAGAGCT
3115	ACGCACACATGGAGACTTGGCTCC	GGAGCCAAGTCTCCATGTGTGCGT
3116	TTCTTGAAAGCTAGTGGGGCGCTA	TAGCGCCCCACTAGCTTTCAAGAA
3117	CAATCACGGCTGGGCTATTCTGTG	CACAGAATAGCCCAGCCGTGATTG
3118	GTGGCGACCCGTCGGTGAAAGAGT	ACTCTTTCACCGACGGGTCGCCAC
3119	CGTCGAATGCCGAACCAGTTAAGT	ACTTAACTGGTTCGGCATTCGACG
3120	TGCGTATTTGCATGCTCACAGCTG	CAGCTGTGAGCATGCAAATACGCA
3121	CGCAGTTGGTTTGTGCACGGCTGC	GCAGCCGTGCACAAACCAACTGCG
3122	GTTTTTCCGTGAAAACTGGCATCG	CGATGCCAGTTTTCACGGAAAAAC
3123	ACAGGTTCCTCCACCACGATTTGA	TCAAATCGTGGTGGAGGAACCTGT
3124	CTAGCGCGCTTTTAGGTCCTTGCG	CGCAAGGACCTAAAAGCGCGCTAG
3125	CAAAATCAAAGGGATCAACCGGTG	CACCGGTTGATCCCTTTGATTTTG
3126	AACGTAACCCCAGTGAGTCAGGCA	TGCCTGACTCACTGGGGTTACGTT
3127	TCAACCGGTGCACTTTAGAACGCC	GGCGTTCTAAAGTGCACCGGTTGA
3128	ATCGCAAAGTTGCAGGCGAATACT	AGTATTCGCCTGCAACTTTGCGAT
3129	ATATGTCCCTGGGTGCTGCACAAC	GTTGTGCAGCACCCAGGGACATAT
3130	TGGCACTTTGTAGTGCTGCGGTGG	CCACCGCAGCACTACAAAGTGCCA
3131	ACGCACGACGTCCTTCTAAGCTCG	CGAGCTTAGAAGGACGTCGTGCGT
3132	CCCACGTGCACTATAGGGATTTCG	CGAAATCCCTATAGTGCACGTGGG
3133	CCGCGCTTGGTCAGTCATCCTTGC	GCAAGGATGACTGACCAAGCGCGG
3134	AGCGGCTCAGGGAATAACAACAGG	CCTGTTGTTATTCCCTGAGCCGCT
3135	ACAACGCGATCGGAGGCAACCAGT	ACTGGTTGCCTCCGATCGCGTTGT
3136	AGCAATTGCCTCCGTAGAAACCCA	TGGGTTTCTACGGAGGCAATTGCT
3137	GAGTCGTGGCATCGCCTGCTATCG	CGATAGCAGGCGATGCCACGACTC
3138	TCTATGCAAATACTGCGCTTGCGA	TCGCAAGCGCAGTATTTGCATAGA
3139	TCAGCTTAAGTTACGGTGTGGCCG	CGGCCACACCGTAACTTAAGCTGA
3140	TCCAAGGTCGAACAGGGATCAGAA	TTCTGATCCCTGTTCGACCTTGGA
3141	GTTAGGCTGGCGTCAATAGCGCTT	AAGCGCTATTGACGCCAGCCTAAC
3142	GGTGTCATAAGGAAGAGGGCATCG	CGATGCCCTCTTCCTTATGACACC
3143	CCGGCGGGCTAGATCAATATTTCT	AGAAATATTGATCTAGCCCGCCGG
3144	CTAACGTCAAGTTTTACGCCCCGA	TCGGGGCGTAAAACTTGACGTTAG
3145	GCAGCACAGTTTTCCGATTTGCGG	CCGCAAATCGGAAAACTGTGCTGC
3146	CGCACGCAAGGGGAGGGATGACTG	CAGTCATCCCTCCCCTTGCGTGCG
3147	CGGGGCCGAAAAGGACGTCACAAG	CTTGTGACGTCCTTTTCGGCCCCG
3148	TTCTCCAACACGGCTAACCGGTAG	CTACCGGTTAGCCGTGTTGGAGAA
3149	TTACAGCCTGGCCCGAGGTAGTTG	CAACTACCTCGGGCCAGGCTGTAA
3150	TTTCGGGCAGCATGAGTTATCGAA	TTCGATAACTCATGCTGCCCGAAA
3151	CTACTGGACGCCCTGCTTCGAAGT	ACTTCGAAGCAGGGCGTCCAGTAG
3152	GGTCGTCCGACGTGAAAAGACCAA	TTGGTCTTTTCACGTCGGACGACC
3153	GTTTTCGAGCTCTTTCTCCGCAGG	CCTGCGGAGAAAGAGCTCGAAAAC

3154	GCGTGAAGGTACCCAGTGTCACAG	CTGTGACACTGGGTACCTTCACGC
3155	TTTCTGAACGCTTCGACGCAACAC	GTGTTGCGTCGAAGCGTTCAGAAA
3156	TGCTAATAAGCACGCCTAGCCCGT	ACGGGCTAGGCGTGCTTATTAGCA
3157	AAATTAATTGTGGTGGCTCCGGCG	CGCCGGAGCCACCACAATTAATTT
3158	TTACAATCCTCGGGCTCACTGACA	TGTCAGTGAGCCCGAGGATTGTAA
3159	GCTGAAGGACAAGGCGTGGGCAAC	GTTGCCCACGCCTTGTCCTTCAGC
3160	GGGATAGGAGACCCTCGCAATGGT	ACCATTGCGAGGGTCTCCTATCCC
3161	TTGCAGTACGTCCTTGCGCATGAA	TTCATGCGCAAGGACGTACTGCAA
3162	TTGATCACTGGATTGGGTGCGAAC	GTTCGCACCCAATCCAGTGATCAA
3163	TCTGCAGACGTTGCGAGAGATGAT	ATCATCTCTCGCAACGTCTGCAGA
3164	AGTCTAGCAGGGATCGAAGCGGAT	ATCCGCTTCGATCCCTGCTAGACT
3165	GGGGTCCCGCAACAACTAATGAAG	CTTCATTAGTTGTTGCGGGACCCC
3166	CAACCTCTTATGTGGTGTGCGCGA	TCGCGCACACCACATAAGAGGTTG
3167	CTCGCTGGGTTGCTGGAGTAGCAC	GTGCTACTCCAGCAACCCAGCGAG
3168	CGTTGTATTGTGCAACGCGAAGTT	AACTTCGCGTTGCACAATACAACG
3169	GGGCTCAAAGTGCCTGAGTCGAAA	TTTCGACTCAGGCACTTTGAGCCC
3170	CTGCTGTGCCCTCTCAGTGAGAGC	GCTCTCACTGAGAGGGCACAGCAG
3171	CGGACGTACTGTTCGGAGTCCTCA	TGAGGACTCCGAACAGTACGTCCG
3172	GTATACCACCATACCGGGACCGCA	TGCGGTCCCGGTATGGTGGTATAC

TABLE 3

Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
17	TTCGCCGTCGTGTAGGCTTTTCAA	TTGAAAAGCCTACACGACGGCGAA
18	GTTCCCAGTGAAGCTGCGATCTGG	CCAGATCGCAGCTTCACTGGGAAC
19	TACTTGGCATGGAATCCCTTACGC	GCGTAAGGGATTCCATGCCAAGTA
20	ACTAGCATATTTCAGGGCACCGGC	GCCGGTGCCCTGAAATATGCTAGT
21	GAACGGTCAATGAACCCGCTGTGA	TCACAGCGGGTTCATTGACCGTTC
22	GCGGCCTTGGTTCAATATGAATCG	CGATTCATATTGAACCAAGGCCGC
23	GATCGTTAGAGGGACCTTGCCCGA	TCGGGCAAGGTCCCTCTAACGATC
24	TGGACCTAGTCCGGCAGTGACGAA	TTCGTCACTGCCGGACTAGGTCCA
25	ATAAACTACCCAGGACGGGCGGAA	TTCCGCCCGTCCTGGGTAGTTTAT
26	CATCGGTTCGCGCCAATCCAGATA	TATCTGGATTGGCGCGAACCGATG
27	GTCGGGCATAGAGCCGACCACCCT	AGGGTGGTCGGCTCTATGCCCGAC
28	CTTGGGTCATGATTCACCGTGCTA	TAGCACGGTGAATCATGACCCAAG
29	TGCCTAACGTGCTAATCAGCAGCG	CGCTGCTGATTAGCACGTTAGGCA
30	CGCATGTTGGAGCATATGCCCTGA	TCAGGGCATATGCTCCAACATGCG
31	AGCCACTGCATCAGTGCTGTTCAA	TTGAACAGCACTGATGCAGTGGCT
32	GGTTGTTTTGAGGCGTCCCACACT	AGTGTGGGACGCCTCAAAACAACC
33	TCGACCAAGAGCAAGGGCGGACCA	TGGTCCGCCCTTGCTCTTGGTCGA
34	GACATCGCTATTGCGCATGGATCA	TGATCCATGCGCAATAGCGATGTC
35	GAAATACGAAGTCTGCGGGAGTCG	CGACTCCCGCAGACTTCGTATTTC
36	TGTCATGAATGATTGATCGCGCGA	TCGCGCGATCAATCATTCATGACA
37	ATATCGGGATTCGTTCCCGGTGAA	TTCACCGGGAACGAATCCCGATAT
38	GCGAGCGTACCGAAGGGCCTAGAA	TTCTAGGCCCTTCGGTACGCTCGC
39	TTACCGGCAGCGGACTTCCGAATT	AATTCGGAAGTCCGCTGCCGGTAA
40	GTAATCGAGAGCTGCGCGCCGTCT	AGACGGCGCGCAGCTCTCGATTAC
41	CCTGTTAGCGTAGGCGAGTCGATC	GATCGACTCGCCTACGCTAACAGG
42	TAGCGGACCGGCAGAATGAGTTCC	GGAACTCATTCTGCCGGTCCGCTA
43	GGTACATGCACTACGCGCACTCGG	CCGAGTGCGCGTAGTGCATGTACC
44	AATTCATCTCGGACTCCCGCGGTA	TACCGCGGGAGTCCGAGATGAATT
45	GCCAAATCTGGATTGGCAGGAATG	CATTCCTGCCAATCCAGATTTGGC
46	TGCATTTTCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
47	CCGCTCAATTCACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
48	CTCGGAAAGGTGCAACTTTGGTGT	ACACCAAAGTTGCACCTTTCCGAG
49	AATTCGACCAGCAGAACGTCCCAT	ATGGGACGTTCTGCTGGTCGAATT
50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCGTGAGGTTGAGACTCTGGC
51	CCAACAACTGGAACGGGAACCCGC	GCGGGTTCCCGTTCCAGTTGTTGG
52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCCTCAGCGATCAGTTCTC
53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC

54	TCACATCCAAATATGGTCCGCGAA	TTCGCGGACCATATTTGGATGTGA
55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTCACACCGGCAGAC
56	CATCGCAGAGCATAAACACCCTCA	TGAGGGTGTTTATGCTCTGCGATG
57	GTTGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATACCAAC
58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
59	GGAATGAGTGGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
60	TGTCAATATGCGTCCGTGTCGTCT	AGACGACACGGACGCATATTGACA
61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCTGAGGCTCATCA
62	CACCGCGGTGTTCCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
64	TTAACCTGCGTCTGCCCCTTTCCT	AGGAAAGGGGCAGACGCAGGTTAA
65	AGGCGCGTTCCTGCCTTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
66	TAGGGCGATGGCACGAAGCTTCAA	TTGAAGCTTCGTGCCATCGCCCTA
67	TGCATAGAGCCAAAGTCGGCGATG	CATCGCCGACTTTGGCTCTATGCA
68	TTGAGAGGCAGGTGGCCACACGGA	TCCGTGTGGCCACCTGCCTCTCAA
69	TCCGCATTGTGAGAAAAAACGAGC	GCTCGTTTTTTCTCACAATGCGGA
70	GGCGGTTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAAACCGCC
71	GGTGAAAATTTCGTAGCCACGGGC	GCCCGTGGCTACGAAATTTTCACC
72	CCGACGGAGGATGAAGACAATCAC	GTGATTGTCTTCATCCTCCGTCGG
73	CCAGTTTGGCCCAATTCGCCAAAA	TTTTGGCGAATTGGGCCAAACTGG
74	GGATCTATTAGGCCGTGCGCACAG	CTGTGCGCACGGCCTAATAGATCC
75	CGGATGTCACCGTTTGGACTTTCA	TGAAAGTCCAAACGGTGACATCCG
76	ATCGCAAATCCTGCTCGTCCCTAA	TTAGGGACGAGCAGGATTTGCGAT
77	CAGGGCATGCAATAATCGAGGTTC	GAACCTCGATTATTGCATGCCCTG
78	CATGCGTTGATATATGGGCCCAAG	CTTGGGCCCATATATCAACGCATG
79	CAGCTGCAGCTTGTGACCAACCAC	GTGGTTGGTCACAAGCTGCAGCTG
80	TTGTATGTCTGCCGACCGGCGACC	GGTCGCCGGTCGGCAGACATACAA
81	GATGGCGCCCGTTGATAGGTATGG	CCATACCTATCAACGGGCGCCATC
82	ATGAGAATCGCCGGCAATCTGCTA	TAGCAGATTGCCGGCGATTCTCAT
83	ATTTGCACTGACCGCAGGCTCGTG	CACGAGCCTGCGGTCAGTGCAAAT
84	CAGGGAGAACGGTTAAGTTCCCGT	ACGGGAACTTAACCGTTCTCCCTG
85	AGGCCGGCGATCGAGGAGTTTGGT	ACCAAACTCCTCGATCGCCGGCCT
86	ACACGGTGGTCTCTGATAGCGACC	GGTCGCTATCAGAGACCACCGTGT
87	GTGCAACGCCGAGGACTTCCATCA	TGATGGAAGTCCTCGGCGTTGCAC
88	TCGGTGCCTGATAGCCATTCCGAT	ATCGGAATGGCTATCAGGCACCGA
89	TGAAATACCACACAGCCAATTGGC	GCCAATTGGCTGTGTGGTATTTCA
90	GCATCGTGTACATGACTGCCGCGA	TCGCGGCAGTCATGTACACGATGC
91	CAGTGTTCTAACGGCGCGCGTGAA	TTCACGCGCGCCGTTAGAACACTG
92	CGCTTGCAACGTTGCACCTACTCT	AGAGTAGGTGCAACGTTGCAAGCG
93	CGAAAAACTAGTGGGCTCGCCGCG	CGCGGCGAGCCCACTAGTTTTTCG
94	CTTTCAGGGGAACTGCCGGAGTCG	CGACTCCGGCAGTTCCCCTGAAAG

95	TTGTGGCCTTCTTGTAAAGGCACG	CGTGCCTTTACAAGAAGGCCACAA
96	TCCACGAACGGCGACCCGTTGTCT	AGACAACGGGTCGCCGTTCGTGGA
97	CGACCTTGCACGAAACCTAACGAG	CTCGTTAGGTTTCGTGCAAGGTCG
98	GTGCAGCTTCACGAGCCAGCCTGA	TCAGGCTGGCTCGTGAAGCTGCAC
99	CGCTTTCGTGCGAATAGACGATGA	TCATCGTCTATTCGCACGAAAGCG
100	TGCGCTTACAGGCTCCTAGTGGTC	GACCACTAGGAGCCTGTAAGCGCA
101	CACGCGCTTAGTCGCGATCGCATA	TATGCGATCGCGACTAAGCGCGTG
102	CGGAGGGAGGGAGCTAGCCTTCGA	TCGAAGGCTAGCTCCCTCCCTCCG
103	GCATCCGGCCTGTTGATGACGCCT	AGGCGTCATCAACAGGCCGGATGC
104	AGGCCAATCGATCTTATTGCCGAG	CTCGGCAATAAGATCGATTGGCCT
105	CCTTCCAATGATTGCATACGCCCA	TGGGCGTATGCAATCATTGGAAGG
106	AACACTTGATCAGGCGGGTCGTCT	AGACGACCCGCCTGATCAAGTGTT
107	TGGAATCAAGGCCGTAAAGGACAG	CTGTCCTTTACGGCCTTGATTCCA
108	GCTCCCGTAACCTGTCCACCAGTG	CACTGGTGGACAGGTTACGGGAGC
109	AGTGGTGAATGGCCGCTACCCTGA	TCAGGGTAGCGGCCATTCACCACT
110	TGTTGAAGCGAGCTAAAACGGCCA	TGGCCGTTTTAGCTCGCTTCAACA
111	CAGCGCTCCAGAATTGACAGCAAT	ATTGCTGTCAATTCTGGAGCGCTG
2	TTCGAAGCGCACGTCCCTTTTCAA	TTGAAAAGGGACGTGCGCTTCGAA
3	AACGCGTGGGGAATGGGACATCAA	TTGATGTCCCATTCCCCACGCGTT
114	CACGAGATACCGGCGTAAGGGTGG	CCACCCTTACGCCGGTATCTCGTG
115	CTACGGCAAACGTGTGGAATGGGT	ACCCATTCCACACGTTTGCCGTAG
116	GTAGGGCGATGACGGGCGAACTAC	GTAGTTCGCCCGTCATCGCCCTAC
117	AATCGACCTCCGCACACATTCGCA	TGCGAATGTGTGCGGAGGTCGATT
118	GAGTCAGCATGGCGGCGGAGATTC	GAATCTCCGCCGCCATGCTGACTC
119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTTGCCAGCGTCTTTATCT
120	GGTACCTCAACGCGAACCACTTGT	ACAAGTGGTTCGCGTTGAGGTACC
121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTTGGGTAGCCATCGCTT
122	AGAGCTTATGCAGAACCAGGCGCC	GGCGCCTGGTTCTGCATAAGCTCT
123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCCTGCGTGAGACCGAT
124	TAGGTTGCCCGCCAGAAGAAACAT	ATGTTTCTTCTGGCGGGCAACCTA
125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTTGCAACAGCACCG
126	TGATGAAAGTTTGCGGCAGGACAC	GTGTCCTGCCGCAAACTTTCATCA
127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
128	AACATTGCGCGGTCCACCAGGGTT	AACCCTGGTGGACCGCGCAATGTT
129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCCC
130	TCGAGCTGGTCCCCGTGAACGTGT	ACACGTTCACGGGGACCAGCTCGA
131	GTCTTGGGGGCCGCTTAGTGAAAA	TTTTCACTAAGCGGCCCCCAAGAC
132	ACTGTTGGCTTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
133	AGGACCATTCGGAAGGCGAAGATA	TATCTTCGCCTTCCGAATGGTCCT
134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCTCCCAAG
135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCCGTTTATT

136	TTGTACGTGCGGTCCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
137	CGCACCAAACTGAGTTTCCCAGAC	GTCTGGGAAACTCAGTTTGGTGCG
138	ACCTGATCGTTCCCCTATTGGGAA	TTCCCAATAGGGGAACGATCAGGT
139	GGAACAGAGGCGAGGGGACTGAGC	GCTCAGTCCCCTCGCCTCTGTTCC
140	CCCTGCCTTGGCGTGTCGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
141	ACTCTGACACGCCAACTCCGGAAG	CTTCCGGAGTTGGCGTGTCAGAGT
142	CTGACGGTTTTCATTCGGCGTGCC	GGCACGCCGAATGAAAACCGTCAG
143	TGCGGTGGTTCATTGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGGCCATGC
145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTCGCTTTACGGCCT
146	CGAATATTATGCCGAGAATCCGCG	CGCGGATTCTCGGCATAATATTCG
147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
148	GGACGGTTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAAACCGTCC
149	AAAGGCTATTGAGTTGGTTGGGCG	CGCCCAACCAACTCAATAGCCTTT
150	GATGGCCTATTCGGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
151	GATCCAGTAGGCAGCTTCATCCCA	TGGGATGAAGCTGCCTACTGGATC
152	AATAACTCGCGCGGGTATGCTTCT	AGAAGCATACCCGCGCGAGTTATT
153	GGAGGAGGTTTGTCTCGGAAAGCA	TGCTTTCCGAGACAAACCTCCTCC
154	CTTTGGTATGGCACATGCTGCCCG	CGGGCAGCATGTGCCATACCAAAG
155	AGAAAGGCTCGAGCAACGGGAACT	AGTTCCCGTTGCTCGAGCCTTTCT
156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCGGACCAGTGCGGTAGATT
157	CGTGGCGGCCACAGTTTTTGGAGG	CCTCCAAAAACTGTGGCCGCCACG
158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGGATTGAACTGCAA
159	GGCCCAAAGCCCCAGACCATTTTA	TAAAATGGTCTGGGGCTTTGGGCC
160	CGCCTGTCTTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG
161	TGAGGCAACAGGGGCCAAAAACTA	TAGTTTTTGGCCCCTGTTGCCTCA
162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAAGCCTTGGGGCC
164	GCACGTGAAGTTTAACCGCGATTC	GAATCGCGGTTAAACTTCACGTGC
165	AGCGGCAGAAACGTTCCTTGACGG	CCGTCAAGGAACGTTTCTGCCGCT
166	TCGTCGAGCAGACGAGATTGCACG	CGTGCAATCTCGTCTGCTCGACGA
167	TCTTTGCCGCGTAACTGACTGCTT	AAGCAGTCAGTTACGCGGCAAAGA
168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTTGGCACATAAA
169	TGTTACTGTGGTTCACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
170	CGCGCCTCGCTAGACCTTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
171	ACAAATGCGTGAGAGCTCCCAACT	AGTTGGGAGCTCTCACGCATTTGT
172	CGCGCAGATTATAGACCCGAATGT	ACATTCGGGTCTATAATCTGCGCG
173	CAAATAACGCCGCTGAATCGGCGT	ACGCCGATTCAGCGGCGTTATTTG
174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTTGCTCGTGTTCA
176	CAGCAGATCCTTCGTAGCGGTCGT	ACGACCGCTACGAAGGATCTGCTG

177	GGAACCTGGTGAGTTGTGCCTCAT	ATGAGGCACAACTCACCAGGTTCC
178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTCGCTTATGA
179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
180	TGTCAGAGCCCGCGACTCAGACGG	CCGTCTGAGTCGCGGGCTCTGACA
181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
182	CTCAGAAGTCCTCGGCGAACTGGG	CCCAGTTCGCCGAGGACTTCTGAG
183	ATCCTTTTATCTACTCCGCGGCGA	TCGCCGCGGAGTAGATAAAAGGAT
184	AGGCGTGCAGCAACAGGATAAACC	GGTTTATCCTGTTGCTGCACGCCT
185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
187	TCCACTATAACTGCGGGTCCGTGT	ACACGGACCCGCAGTTATAGTGGA
188	GCCCAGTCGGCTCTAACAAGTTCG	CGAACTTGTTAGAGCCGACTGGGC
189	CGGAACGGATAATCGGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
190	TAAAATAAGCGCCTGGCGGGAGGA	TCCTCCCGCCAGGCGCTTATTTTA
191	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC
192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAACT
193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
194	TTCGCAGCACCCGCTAGGTACAGT	ACTGTACCTAGCGGGTGCTGCGAA
195	TAACCCGATTTTTGCGACTCTGCC	GGCAGAGTCGCAAAAATCGGGTTA
196	CGTCGCATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCAATGCGACG
197	GAGCTGACGTCACCATCAGAGGAA	TTCCTCTGATGGTGACGTCAGCTC
198	GGAGGCTGGGGGTCGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
199	TTGTGGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCCACAA
200	CCCTCGCACTGTGTTCACCCTCTT	AAGAGGGTGAACACAGTGCGAGGG
201	TCATTGACTCGAATCCGCACAACG	CGTTGTGCGGATTCGAGTCAATGA
202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTCGTTTCATGTCCGCGC
206	CTTATTGGGTGCCGGTGTCGGATT	AATCCGACACCGGCACCCAATAAG
207	GGGGCGGTTACCAAAAATCCGAT	ATCGGATTTTTGGTAACCGCCCC
4	CCGTCGCATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
5	ATGGCCGTGCTGGGGACAAGTCAA	TTGACTTGTCCCCAGCACGGCCAT
210	ACGAAAAAAGTGTGCGGATCCCCT	AGGGGATCCGCACACTTTTTTCGT
211	CCAAGTACACCGCACGCATGTTTA	TAAACATGCGTGCGGTGTACTTGG
212	ATCGTGCGTGGAGTGTCGCATCTA	TAGATGCGACACTCCACGCACGAT
213	TCCAGATACCGCCCCGAACTTTGA	TCAAAGTTCGGGGCGGTATCTGGA
214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
215	TTGAAATTGCTCTGCCGTCAGTCA	TGACTGACGGCAGAGCAATTTCAA
216	AGTCAGGCGAGATGTTCAGGCAGC	GCTGCCTGAACATCTCGCCTGACT
217	ACAAGCCGACGTTAAGCCCGCCCA	TGGGCGGGCTTAACGTCGGCTTGT

218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
219	GTGAGACACACATCCCCTCCAATG	CATTGGAGGGGATGTGTGTCTCAC
220	CGACGGATGCAGAGTTCAGTGGTC	GACCACTGAACTCTGCATCCGTCG
221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
222	TTAGCAAAGCGGCGCCGTTAGCAA	TTGCTAACGGCGCCGCTTTGCTAA
223	CCCGACACGGGTCAGCGTAATAAT	ATTATTACGCTGACCCGTGTCGGG
224	GCGACGGCCCTGAGGTATGTCGTC	GACGACATACCTCAGGGCCGTCGC
225	CAAAAGTGTGTTCCCTTGCGCTTG	CAAGCGCAAGGGAACACACTTTTG
226	TCTCGAAGCACAGCCCGGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
227	ATGCTAACCGTTGGCCATGGAACT	AGTTCCATGGCCAACGGTTAGCAT
228	CTTGCGGAGTGTTAGCCCAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA
230	CCAATGCCTTTGAGTAAGCGATGG	CCATCGCTTACTCAAAGGCATTGG
231	AGCAGATAACGTCCCAATGACGCC	GGCGTCATTGGGACGTTATCTGCT
232	TTGACCATTACGTGTTGCGCCCAT	ATGGGCGCAACACGTAATGGTCAA
233	TCGCGTATTTGCGGAATTCGTCTG	CAGACGAATTCCGCAAATACGCGA
234	CTGCGTGTCAACAATGTCCCGCAG	CTGCGGGACATTGTTGACACGCAG
235	TCTGGTGCCACGCAAGGTCCACAG	CTGTGGACCTTGCGTGGCACCAGA
236	CTCCGGGAGGTCACTTAATTGCGG	CCGCAATTAAGTGACCTCCCGGAG
237	TTTTCGTGATTGCCCGGAGGAGGC	GCCTCCTCCGGGCAATCACGAAAA
238	TCGGGATGTAGCTGGGGCTACCGG	CCGGTAGCCCCAGCTACATCCCGA
239	CGAGCCAACGCAAACACGTCCTTG	CAAGGACGTGTTTGCGTTGGCTCG
240	GCAAAGCCTTTGTGGGGCGGTAGT	ACTACCGCCCCACAAAGGCTTTGC
241	ATTCGACCGGAAATGAGGTCTTCG	CGAAGACCTCATTTCCGGTCGAAT
242	TTCGCTTGCTGAGTTGCTCTGTTC	GAACAGAGCAACTCAGCAAGCGAA
243	CGCGTGAAGACCCCATTCCCGAGT	ACTCGGGAATGGGGTCTTCACGCG
244	AACCGTATTCGCGGTCACTTGTGG	CCACAAGTGACCGCGAATACGGTT
245	GGGGCCAACCGTTTCGAGGCGTAT	ATACGCCTCGAAACGGTTGGCCCC
246	TTCGGCTGGCAGTCCAAACGGCTT	AAGCCGTTTGGACTGCCAGCCGAA
247	GGGTGTGGTTAGAATGCACGGTTC	GAACCGTGCATTCTAACCACACCC
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250	TAAAAGGTCGCTTTGAAAGGGGGA	TCCCCCTTTCAAAGCGACCTTTTA
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253	ATGCTGACATGTCGTGCACCTCGT	ACGAGGTGCACGACATGTCAGCAT
254	TGTGGTTAAAGCGTCCGTTCAACG	CGTTGAACGGACGCTTTAACCACA
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256	CCTATCCCGGCGAGAACTTCTGTG	CACAGAAGTTCTCGCCGGGATAGG
257	GTCTGCACTCACGCAGCGGAGGGA	TCCCTCCGCTGCGTGAGTGCAGAC
258	GCACGAGTTGGTGCTCGGCAGATT	AATCTGCCGAGCACCAACTCGTGC

259	AACGTCGCACGACACACGTTCGTC	GACGAACGTGTGTCGTGCGACGTT
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262	TGTGCCTCATCCTTAGGATACGGC	GCCGTATCCTAAGGATGAGGCACA
263	AGGTGGTGTGGGTCAACCGCTTTA	TAAAGCGGTTGACCCACACCACCT
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265	TAGATCAACTCGCGTACGCATGGA	TCCATGCGTACGCGAGTTGATCTA
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267	TACGTGTGGAGATGCCCCGAACCG	CGGTTCGGGGCATCTCCACACGTA
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269	AGCGAGGTTTCTAGCGTCGACACC	GGTGTCGACGCTAGAAACCTCGCT
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272	AGGCCGATTTCACCCGCCAATTGC	GCAATTGGCGGGTGAAATCGGCCT
273	GAGCCCTCACTCCTTGCCCTTTGA	TCAAAGGGCAAGGAGTGAGGGCTC
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276	TCGACGTTAGGAGTGCTGCCAGAA	TTCTGGCAGCACTCCTAACGTCGA
277	CGAATGGGTCTGGACCTTGCATAG	CTATGCAAGGTCCAGACCCATTCG
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281	AAGGCTCAACACGCCTATGTGCGC	GCGCACATAGGCGTGTTGAGCCTT
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296	CATAAAAAAACCTGGGGCTCTGCG	CGCAGAGCCCCAGGTTTTTTTATG
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503	GAGACGCTGTCACTCCGGCAGAAC	GTTCTGCCGGAGTGACAGCGTCTC
504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG

505	CGGCATAACGTCCAGTCCTGGGAC	GTCCCAGGACTGGACGTTATGCCG
506	AAGCGGAACGGGTTATACCGAGGT	ACCTCGGTATAACCCGTTCCGCTT
507	TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
508	AGGGAACCGCGTTCAAACTCAGTT	AACTGAGTTTGAACGCGGTTCCCT
509	GAATTACAACCACCCGCTCGTGTT	AACACGAGCGGGTGGTTGTAATTC
510	TTCAGTGCTCACGAAGCATGGATT	AATCCATGCTTCGTGAGCACTGAA
511	TTAGTTTGGCGTTGGGACTTCACC	GGTGAAGTCCCAACGCCAAACTAA
512	AATGCGACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
513	CCGAAACCGTTAACGTGGCGCACA	TGTGCGCCACGTTAACGGTTTCGG
514	TAAAGTAACAAGGCGACCTCCCGC	GCGGGAGGTCGCCTTGTTACTTTA
515	TAATGATTTTAGTCGCGGGGTGGG	CCCACCCCGCGACTAAAATCATTA
516	GGCTACTCTAAGTGCCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCCGCCA
518	GGGCGTTAGGCGTAATAGACCGTC	GACGGTCTATTACGCCTAACGCCC
519	GCCACCTTTAGACGGCGGCTCTAG	CTAGAGCCGCCGTCTAAAGGTGGC
520	GAGATGTGTAAACGTGCAGGCACC	GGTGCCTGCACGTTTACACATCTC
521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGGAGGGCCACGAGCTA
522	GTGTCGGCGCTATTTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
523	CCAGGGAAGCAACTGGTTGCCATT	AATGGCAACCAGTTGCTTCCCTGG
524	TTCCGAAACTAAGCCAGAACCGCT	AGCGGTTCTGGCTTAGTTTCGGAA
525	GCAAACCCGGTAACCCGAGAGTTC	GAACTCTCGGGTTACCGGGTTTGC
526	GCAAATGGCGTCATGCACGAACGT	ACGTTCGTGCATGACGCCATTTGC
527	AGTACTTTCGCGCCCAGTTTAGGG	CCCTAAACTGGGCGCGAAAGTACT
528	AAGATCTGCGAGGCATCCCGGCTT	AAGCCGGGATGCCTCGCAGATCTT
529	GCAAGTGTATCGCACAGTGCGATT	AATCGCACTGTGCGATACACTTGC
530	CCGACAAGGCCTCAATTCATTCTG	CAGAATGAATTGAGGCCTTGTCGG
531	GTCTCGTCTCAACTTTAAGGCGCG	CGCGCCTTAAAGTTGAGACGAGAC
532	ATCCAGAGATCCGTTTTGCAGCGT	ACGCTGCAAAACGGATCTCTGGAT
533	GTCACCAGGAGGGAAGTTTCACCC	GGGTGAAACTTCCCTCCTGGTGAC
534	TTCCGTCAGGCGGATCAACGGAAT	ATTCCGTTGATCCGCCTGACGGAA
535	ATGCCGGACACGCATTACACAGGC	GCCTGTGTAATGCGTGTCCGGCAT
536	TGGGCCGCTTGGCGCTTTCATAGA	TCTATGAAAGCGCCAAGCGGCCCA
537	CCTAGCGCGAGCTTTACTGACCAG	CTGGTCAGTAAAGCTCGCGCTAGG
538	TTGGCCAGGAATATGGTCTCGAGA	TCTCGAGACCATATTCCTGGCCAA
539	GTCTGCGGCCGACTTGCTATGCAT	ATGCATAGCAAGTCGGCCGCAGAC
540	AACTTGCTCATTCTCAAGCCGACG	CGTCGGCTTGAGAATGAGCAAGTT
541	ACGTCAGCGATTGTGGCGAAATAT	ATATTTCGCCACAATCGCTGACGT
542	ACGGCCTGCGTCAGCACATGCATC	GATGCATGTGCTGACGCAGGCCGT
543	ATACCTCCGCAGAACCATTCCGTT	AACGGAATGGTTCTGCGGAGGTAT
544	AGTTCGCGGTCCCACGATTCACTT	AAGTGAATCGTGGGACCGCGAACT
545	TGCTCAATTTGTGCAGAAAACGCC	GGCGTTTTCTGCACAAATTGAGCA

546	TTATCGCGAGAGACGACCGTGTCC	GGACACGGTCGTCTCTCGCGATAA
547	GACGCGACGTGAGTAGTGGAAGCG	CGCTTCCACTACTCACGTCGCGTC
548	ATGGTAGGGGCATTGGGCTTTCCT	AGGAAAGCCCAATGCCCCTACCAT
549	CCAAATATAGCCGCGCGGAGACAT	ATGTCTCCGCGCGGCTATATTTGG
550	GCAAACCCTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTTGC
551	TAGCGTCTTGCGTGAAACCATGGG	CCCATGGTTTCACGCAAGACGCTA
552	CCACCCCGACAGCGCTGGACTCTT	AAGAGTCCAGCGCTGTCGGGGTGG
553	ACGAGCACTGAAGGCTGCTTTACG	CGTAAAGCAGCCTTCAGTGCTCGT
554	CATATCAGCGTCGTCTAGCTCGCG	CGCGAGCTAGACGACGCTGATATG
555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
556	GGCCCCGACACTACAGGGTAATCA	TGATTACCCTGTAGTGTCGGGGCC
557	GGCTCCAGGGCGAGATTATGAATG	CATTCATAATCTCGCCCTGGAGCC
558	CAAAATCCGATGGGCGGAAAATTA	TAATTTTCCGCCCATCGGATTTTG
559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
560	TAGCTATTGCCCCGATGGGCTACT	AGTAGCCCATCGGGGCAATAGCTA
561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
562	GACGCTGTGGCTCGGAAACTGTTC	GAACAGTTTCCGAGCCACAGCGTC
563	CCTGGGTTCGCCGCGTGGTAACTG	CAGTTACCACGCGGCGAACCCAGG
564	TTCCCGCGTAGCCCAACAGCTATA	TATAGCTGTTGGGCTACGCGGGAA
565	TTCGCGGATTGCTGCCGCATAACA	TGTTATGCGGCAGCAATCCGCGAA
566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTTCGGTGCCATTTTT
567	CATTCCGCGCGAGTTGAAATCCAG	CTGGATTTCAACTCGCGCGGAATG
568	ACGCACGTTTTTTGGCACGGTTAA	TTAACCGTGCCAAAAAACGTGCGT
569	TGTCCATGACGTCGTTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
570	TCTCAGTCGGACTCGTATGCCAGA	TCTGGCATACGAGTCCGACTGAGA
571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGTGCGTTTGGAG
572	TTCAACCAAGCGGGGTGTTCGTGA	TCACGAACACCCCGCTTGGTTGAA
573	GGTGTCGGAGGGTGGTGACCTCGA	TCGAGGTCACCACCCTCCGACACC
574	AGCGCTTTTGGTCATGATTTGCAA	TTGCAAATCATGACCAAAAGCGCT
575	CCGAGGACTTACGTCTGCCCAGGA	TCCTGGGCAGACGTAAGTCCTCGG
576	GCCCAATCCAGTTCTTATGCGCCC	GGGCGCATAAGAACTGGATTGGGC
577	CGGGTTAACCCACGCAAGTTATGA	TCATAACTTGCGTGGGTTAACCCG
578	TGATTAGCGCTCAATACACGCGTG	CACGCGTGTATTGAGCGCTAATCA
579	AAGGGCAGACCTTTGGTTCGACTG	CAGTCGAACCAAAGGTCTGCCCTT
580	GCGCCACAAGATTCACATGTCATT	AATGACATGTGAATCTTGTGGCGC
581	GCCATGTTCAAGGGCCTTTCGAAG	CTTCGAAAGGCCCTTGAACATGGC
582	CGCGGTGTTTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
584	CGATACGCGCCGGTTTGTTAAATC	GATTTAACAAACCGGCGCGTATCG
585	GGCTATAAACGTGCGGACTGCTCC	GGAGCAGTCCGCACGTTTATAGCC
586	TGGGTAAATCACTATTGCGCGGTT	AACCGCGCAATAGTGATTTACCCA

587	GTCTTCATCGGCCCGCGCAAGCTA	TAGCTTGCGCGGGCCGATGAAGAC
588	GCGACACACCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCGC
589	GTAGCAGGGTCCGCAAGACCAAGC	GCTTGGTCTTGCGGACCCTGCTAC
590	TCGCCAACGCAGGGTAACTGCCAT	ATGGCAGTTACCCTGCGTTGGCGA
591	ACTCCGAAGCTTCGAGCGGCACGA	TCGTGCCGCTCGAAGCTTCGGAGT
12	CATCGTCCCTTTCGATGGGATCAA	TTGATCCCATCGAAAGGGACGATG
13	GCACGGGAGCTGACGACGTGTCAA	TTGACACGTCGTCAGCTCCCGTGC
594	ATCATCCCACGGCAGAGTGAAGAG	CTCTTCACTCTGCCGTGGGATGAT
595	CGCTGGACTGGCCTATCCGAGTCG	CGACTCGGATAGGCCAGTCCAGCG
596	CGGTCTCAGCAACACTGTCGCAAA	TTTGCGACAGTGTTGCTGAGACCG
597	CGAACGTTCTCCGATGTAATGGCC	GGCCATTACATCGGAGAACGTTCG
598	ATACCGTGCGACAAGCCCCTCTGA	TCAGAGGGGCTTGTCGCACGGTAT
599	AGCTCATTCCCGAGACGGAACACC	GGTGTTCCGTCTCGGGAATGAGCT
600	TTTCATGCGGCCGTTGCAAATCAT	ATGATTTGCAACGGCCGCATGAAA
601	ACTCGAACGGACGTTCAATTCCCA	TGGGAATTGAACGTCCGTTCGAGT
602	CTGCATGGTGTGGGTGAGACTCCC	GGGAGTCTCACCCACACCATGCAG
603	CCGCGAGTGTGGATGGCGTGTTGA	TCAACACGCCATCCACACTCGCGG
604	AATGTGTCGGTCCTAAGCCGGGTG	CACCCGGCTTAGGACCGACACATT
605	TAAGACGAGCCTGCACAGCTTGCG	CGCAAGCTGTGCAGGCTCGTCTTA
606	GGCGTGGGAGGATAAGACGATGTC	GACATCGTCTTATCCTCCCACGCC
607	TGCTCCATGTTAGGAACGCACCAC	GTGGTGCGTTCCTAACATGGAGCA
608	CGGTGTTGGTCGGACTGACGACTG	CAGTCGTCAGTCCGACCAACACCG
609	CCGCGCGTATCTATCAGATCTGGG	CCCAGATCTGATAGATACGCGCGG
610	AAAGCATGCTCCACCTGGAGCGAG	CTCGCTCCAGGTGGAGCATGCTTT
611	ACTTGCATCGCTGGGTAGATCCGG	CCGGATCTACCCAGCGATGCAAGT
612	TGCTTACGCAGTGGATTGGTCAGA	TCTGACCAATCCACTGCGTAAGCA
613	ATGCAGATGAACAAATCGCCGAAT	ATTCGGCGATTTGTTCATCTGCAT
614	GCAATTCTGGGCCATGTATTCGTC	GACGAATACATGGCCCAGAATTGC
615	AGGGTTCCTTACGCGTCGACATGG	CCATGTCGACGCGTAAGGAACCCT
616	GTGGAGCTAATCGCGAGCCTCAGA	TCTGAGGCTCGCGATTAGCTCCAC
617	TCGTAGTCTCACCGGCAATGATCC	GGATCATTGCCGGTGAGACTACGA
618	TTATAGCAGTGCGCCAATGCTTCG	CGAAGCATTGGCGCACTGCTATAA
619	CGAACAGTGCTGTCCGTCGCTCAA	TTGAGCGACGGACAGCACTGTTCG
620	TCCGCGTGGACTGTTAGACGCTAT	ATAGCGTCTAACAGTCCACGCGGA
621	CATTAGCCCGCTGTCGGTAACTGT	ACAGTTACCGACAGCGGGCTAATG
622	GGAAAGAAACTCAGACGCGCAATG	CATTGCGCGTCTGAGTTTCTTTCC
623	CGACTCGCTGGACAGGAGAATCGT	ACGATTCTCCTGTCCAGCGAGTCG
624	CATGATCCTCTGTTTCACCCGCGG	CCGCGGGTGAAACAGAGGATCATG
625	GGCGTAGCGCTCTAAAAGCTTCGG	CCGAAGCTTTTAGAGCGCTACGCC
626	AGTGATGCCATCAGGCCCGTATAC	GTATACGGGCCTGATGGCATCACT
627	TATGGAAAGGGCAACAGCGCTATC	GATAGCGCTGTTGCCCTTTCCATA

628	CTGTGGTTGATGGAGGATCCACAC	GTGTGGATCCTCCATCAACCACAG
629	ACTCGCTGGAATTTGCGCTGACAC	GTGTCAGCGCAAATTCCAGCGAGT
630	CAGGCCCGAACCACGCGGTTACAG	CTGTAACCGCGTGGTTCGGGCCTG
631	GGCGCAATGGGCGCATAAATACTA	TAGTATTTATGCGCCCATTGCGCC
632	GGTCAATTCGCGCTACATGCCCTA	TAGGGCATGTAGCGCGAATTGACC
633	GATGGTGGACTGGAGCCCTTCCGC	GCGGAAGGGCTCCAGTCCACCATC
634	CCGCGCATAGCGCAATAGGGGAGA	TCTCCCCTATTGCGCTATGCGCGG
635	TCTTCTGGCTGTCCGGCACCCGAA	TTCGGGTGCCGGACAGCCAGAAGA
636	GCGTTCGCAATTCACGGGCCCTTA	TAAGGGCCCGTGAATTGCGAACGC
637	TCGTTTCGGCCTTGGAGAGTATCG	CGATACTCTCCAAGGCCGAAACGA
638	AGGTGCAAGTGCAAGGCGAGAGGC	GCCTCTCGCCTTGCACTTGCACCT
639	CGCCAGTTTCGATGGCTGACGTTT	AAACGTCAGCCATCGAAACTGGCG
640	GCTTTACCGCCGATCCCAGATATC	GATATCTGGGATCGGCGGTAAAGC
641	GTGCTTGACGAAGAGGCGAAATGT	ACATTTCGCCTCTTCGTCAAGCAC
642	CAGTCCGTGCGCTTCATGTCCTCA	TGAGGACATGAAGCGCACGGACTG
643	TACGCGTAAGAGCCTACCCTCGCG	CGCGAGGGTAGGCTCTTACGCGTA
644	GGCGAGTCTTGTGGGGACATGTGT	ACACATGTCCCCACAAGACTCGCC
645	CCAAAGCGAAGCGAGCGTGTCTAT	ATAGACACGCTCGCTTCGCTTTGG
646	GCCGTAGGTTGCTCTTCACCGAAC	GTTCGGTGAAGAGCAACCTACGGC
647	AAATCCGCGATGTGCCGTGAGGCT	AGCCTCACGGCACATCGCGGATTT
648	GGCTTCGCACCCGTACCAATTTAG	CTAAATTGGTACGGGTGCGAAGCC
649	TGTAGAGTCCCACGTAGCCGGCAT	ATGCCGGCTACGTGGGACTCTACA
650	CACTAGTCTGGGGCAAGGTGCATT	AATGCACCTTGCCCCAGACTAGTG
651	TGTACTCGGCAGGCGCAATAGATT	AATCTATTGCGCCTGCCGAGTACA
652	AACGGGTATCGGAAGCGTAAAAGC	GCTTTTACGCTTCCGATACCCGTT
653	CGGACTGCCCGTTTGCAAGTTGAG	CTCAACTTGCAAACGGGCAGTCCG
654	ATCGTTCAGCACTGGAGCCCGTAA	TTACGGGCTCCAGTGCTGAACGAT
655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTTCGATGCAT
656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCCTTAATGCCTGGAA
657	GTGCGACATCTACTCCACGATCCC	GGGATCGTGGAGTAGATGTCGCAC
658	CTCATCGTCCTAACACGAGAGCCC	GGGCTCTCGTGTTAGGACGATGAG
659	AATGGCACTTCGGCGGTGATGCAA	TTGCATCACCGCCGAAGTGCCATT
660	CCGTGGGAGGGAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCCACGG
661	AAATTCTCGTTGGTGACGGCTCAT	ATGAGCCGTCACCAACGAGAATTT
662	TTGCTCTTATCCTTGTCCTGGGCG	CGCCCAGGACAAGGATAAGAGCAA
663	TTAAGGATCAGGCGGAGCTTGCAG	CTGCAAGCTCCGCCTGATCCTTAA
664	CGCGACTAAGGTGCTGCAACTCGA	TCGAGTTGCAGCACCTTAGTCGCG
665	GCTCGATTTCACGGCCCGTTGTTC	GAACAACGGGCCGTGAAATCGAGC
666	AGCAGAGTGCGTTGCAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
667	TGGAGGTGAGGACGACGTGCACTA	TAGTGCACGTCGTCCTCACCTCCA
668	AACCGTTTAGGGTACATTCGCGGT	ACCGCGAATGTACCCTAAACGGTT

669	TATGATCGCTCGGCTCACAGTTTG	CAAACTGTGAGCCGAGCGATCATA
670	GACTTTTTGCGGAAACGTCATGGT	ACCATGACGTTTCCGCAAAAAGTC
671	TGTCGGTTATTCCACCTGCAAGGA	TCCTTGCAGGTGGAATAACCGACA
672	CTATGGTTTGCACTGCGCCGTCGA	TCGACGGCGCAGTGCAAACCATAG
673	AGCAGGGAAATTCAATCGTTCGCA	TGCGAACGATTGAATTTCCCTGCT
674	CCTAACCGAGCGCTTAGCATTTCC	GGAAATGCTAAGCGCTCGGTTAGG
675	CCCGACCCTAACTCGCATTGAATA	TATTCAATGCGAGTTAGGGTCGGG
676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATTAAGCAA
677	GATGCTCGCCGTGTTTAGTTCACG	CGTGAACTAAACACGGCGAGCATC
678	TCGGATGACGAGTTTCCATGACGG	CCGTCATGGAAACTCGTCATCCGA
679	ATGCGGTCTACTTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
680	TTGCGAGGCTAAGCACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
681	AACTTAATTACCGCCTCTGGCGCC	GGCGCCAGAGGCGGTAATTAAGTT
682	GTGACCGCGAACTTGTTCCGACAG	CTGTCGGAACAAGTTCGCGGTCAC
683	TGCGGATTACCGATTCGCTCTTAA	TTAAGAGCGAATCGGTAATCCGCA
684	TGATAGGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCCTATCA
685	TCGCTCCGTAGCGATTCATCGTAG	CTACGATGAATCGCTACGGAGCGA
686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGGAGGCTACCAGCTGACA
687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAAGCGTCATGCGACGCT
14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
15	CGTGTAGGGGTCCCGTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGCAGAATGCGAC
691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTCACCCAAGGTCCCTT
693	TCAAATGGCCACCGCGTGTCATTC	GAATGACACGCGGTGGCCATTTGA
694	CTCCGACGACCAATAAATAGCCGC	GCGGCTATTTATTGGTCGTCGGAG
695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTCTACGGGAATAGCC
696	TGGATAACCTCTCGGTCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
697	GACCGCTGTACGGGAGTGTGCCTT	AAGGCACACTCCCGTACAGCGGTC
698	GCCACAGAGTTTTAGCAGGGACCC	GGGTCCCTGCTAAAACTCTGTGGC
699	CCCACGCTTTCCGACCACTGACCT	AGGTCAGTGGTCGGAAAGCGTGGG
700	CATTGACACAATGCGGGGACTGAT	ATCAGTCCCCGCATTGTGTCAATG
701	AGCCACTCGACAGGGTTCCAAAGC	GCTTTGGAACCCTGTCGAGTGGCT
702	CAGGATGAGCAAAGCGACTCTCCA	TGGAGAGTCGCTTTGCTCATCCTG
703	CAAGGTATGGTCTGGGGCCTAAGC	GCTTAGGCCCCAGACCATACCTTG
704	GGTGTTCGGCCTAAACTCTTTCGG	CCGAAAGAGTTTAGGCCGAACACC
705	TTTAGTCGGACCCTGTGGCAATTC	GAATTGCCACAGGGTCCGACTAAA
706	CACACGTTTCCGACCAGCCTGAAC	GTTCAGGCTGGTCGGAAACGTGTG
707	CTGGACGAACTGGCTTCCTCGTAC	GTACGAGGAAGCCAGTTCGTCCAG
708	TTCACAATCCGCCGAAAACTGACC	GGTCAGTTTTCGGCGGATTGTGAA
709	AACAGGATATCCGCGATCACGACA	TGTCGTGATCGCGGATATCCTGTT

710	TACGTCGGATCCATTGCGCCGAGT	ACTCGGCGCAATGGATCCGACGTA
711	CATGGATCTCTCGGTTTGATCGCC	GGCGATCAAACCGAGAGATCCATG
712	AGCCAGGCGCGTATATACGCTCGG	CCGAGCGTATATACGCGCCTGGCT
713	ATTTGGCACGTGTCGTGCCATGTT	AACATGGCACGACACGTGCCAAAT
714	CCGCGTTGCACCACTTTGAGGTGC	GCACCTCAAAGTGGTGCAACGCGG
715	TTGGACGTGACAAGCATGGCGCTC	GAGCGCCATGCTTGTCACGTCCAA
716	CTGAATCGCGCAAGTAAATGGGGG	CCCCCATTTACTTGCGCGATTCAG
717	GATAAGGTCCACCAGATTGCGCGC	GCGCGCAATCTGGTGGACCTTATC
718	CTAACAATTGCCAACCGGGACGGC	GCCGTCCCGGTTGGCAATTGTTAG
719	GGTAACCTGGGTGCTTGCAGGTTA	TAACCTGCAAGCACCCAGGTTACC
720	ATCGGAGCCACCATTCGCATTGGG	CCCAATGCGAATGGTGGCTCCGAT
721	GTGAACTGGCTTGCCCCAGGATTA	TAATCCTGGGGCAAGCCAGTTCAC
722	AGGCGATAGCATGGTCCCATATGA	TCATATGGGACCATGCTATCGCCT
723	AACGGTATCGTGGCTAATGCACGA	TCGTGCATTAGCCACGATACCGTT
724	AGTAGTGGTCCTCCAGATCGGCAA	TTGCCGATCTGGAGGACCACTACT
725	CCGTTGAATTGGACGGGAGGTTAG	CTAACCTCCCGTCCAATTCAACGG
726	GCATAAGTGCGGCATCGCGAAGGG	CCCTTCGCGATGCCGCACTTATGC
727	CGACAAGATGCAGCTGCTACATGC	GCATGTAGCAGCTGCATCTTGTCG
728	TCGCAGTGATTCCCGACCGATAAG	CTTATCGGTCGGGAATCACTGCGA
729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCTCGAGTGGACTCGCCTTG
730	GCAACTTGCACGGCATAAGTGGCC	GGCCACTTATGCCGTGCAAGTTGC
731	TCCGAGCTTGACGTTCGCGACGTC	GACGTCGCGAACGTCAAGCTCGGA
732	AGCGCTGGGCTGTGCTGCCATCTC	GAGATGGCAGCACAGCCCAGCGCT
733	TTCATGTCGCTGAGTAACCCTCGC	GCGAGGGTTACTCAGCGACATGAA
734	CGAACCGCTAATGCCCATTGTCAG	CTGACAATGGGCATTAGCGGTTCG
735	CACGGAAGGTGGGACAAATCGCCG	CGGCGATTTGTCCCACCTTCCGTG
736	CACAGATGGAGACAAACGCGCCTT	AAGGCGCGTTTGTCTCCATCTGTG
737	TTTTCGCAACTCGCTCCATAACCC	GGGTTATGGAGCGAGTTGCGAAAA
738	ACGTTACGTTTCCGGCGCCTCTAA	TTAGAGGCGCCGGAAACGTAACGT
739	TATCGGATTGCGTGGGTTTCAATC	GATTGAAACCCACGCAATCCGATA
740	CTTCCACAATTGTCTGCGACGCAC	GTGCGTCGCAGACAATTGTGGAAG
741	TGCACAAAGGTATGGCTGTCCGGC	GCCGGACAGCCATACCTTTGTGCA
742	TCCGATGCCAGTCCCATCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
743	CTGAAACCGTGCGAATCGAGGTGA	TCACCTCGATTCGCACGGTTTCAG
744	CGGTGTTCCGCGTGTCGAAAAAAT	ATTTTTTCGACACGCGGAACACCG
745	TCTAGCAGGCCTTTTGAATCGCCA	TGGCGATTCAAAAGGCCTGCTAGA
746	GAGTCACCTCTGAGACGGACGCCA	TGGCGTCCGTCTCAGAGGTGACTC
747	TCTTCTGTCATCCTGCAGCAGCAT	ATGCTGCTGCAGGATGACAGAAGA
748	GCGGATGAAACCTGAAAGGGGCCT	AGGCCCCTTTCAGGTTTCATCCGC
749	GGGGCCCCAAACTGGTATCAAGCC	GGCTTGATACCAGTTTGGGGCCCC
750	GCATTGGCTTCGGATTCTCCTACA	TGTAGGAGAATCCGAAGCCAATGC

751	AGGCGGCCCAACTGTGAGGTCTTG	CAAGACCTCACAGTTGGGCCGCCT
752	ACACCATGTGCTCCGCGCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
753	ACGATGAACATGAATCGGGAGTCG	CGACTCCCGATTCATGTTCATCGT
754	CTGCATCCCTGTAGCAGCGCTCCG	CGGAGCGCTGCTACAGGGATGCAG
755	GTGCCGTATTTCGACCTGTGCGTT	AACGCACAGGTCGAAATACGGCAC
756	GCAGTGCGCACTTCAGTTCAAAAG	CTTTTGAACTGAAGTGCGCACTGC
757	GCGATTTTAAGCGATGCCTTGACG	CGTCAAGGCATCGCTTAAAATCGC
758	TAGGTGACCTAGGCTTGCTTGCGG	CCGCAAGCAAGCCTAGGTCACCTA
759	CTGGATACCTTGCCTGTGCGGCGC	GCGCCGCACAGGCAAGGTATCCAG
760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
761	GCGCTTGCCCGATGCGATGCATTA	TAATGCATCGCATCGGGCAAGCGC
762	TTTCTGTAAGCGGCCTGGGGTTCA	TGAACCCCAGGCCGCTTACAGAAA
763	GGCTGAGGTGAGCGGTAAGGATGA	TCATCCTTACCGCTCACCTCAGCC
764	TCTTGGCCTCCCCGATCTAATTTG	CAAATTAGATCGGGGAGGCCAAGA
765	GGAGGTAACGCCGTGTACGTAGGA	TCCTACGTACACGGCGTTACCTCC
766	GTAATCCATTTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
767	CAAACCCATTCCAGCAGACGCCTG	CAGGCGTCTGCTGGAATGGGTTTG
768	TAGGAGGAATTTGGCATGCGGGCG	CGCCCGCATGCCAAATTCCTCCTA
769	ATAGGTAGGATGTGCCCGGCGTTG	CAACGCCGGGCACATCCTACCTAT
770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAAGCACTTGC
771	CTGGCTGTGTCGCATCTCGTTAAC	GTTAACGAGATGCGACACAGCCAG
772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
773	TTTTCATAAACGTTGTCCCCGAGC	GCTCGGGGACAACGTTTATGAAAA
774	AGCAGGAGGACGAACCTCCGCTCC	GGAGCGGAGGTTCGTCCTCCTGCT
775	TTCAAGCACCATCGTGCAATCCAA	TTGGATTGCACGATGGTGCTTGAA
776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
777	TACATTCCCTGCCTCCGTGGGCTT	AAGCCCACGGAGGCAGGGAATGTA
778	CGCTTCGCGTATTCAGTAGCGGTT	AACCGCTACTGAATACGCGAAGCG
779	TCGGACGCGTCGACACTCATTATA	TATAATGAGTGTCGACGCGTCCGA
780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCCTGCTCAGA
781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAGGGCTTGGCAATTCAA
782	AGTTTTCGCCTTGATGCGTCGGTG	CACCGACGCATCAAGGCGAAAACT
783	GTTTCATAGGCCACGCGTGCTAAA	TTTAGCACGCGTGGCCTATGAAAC
16	CATCGCTGCAAGTACCGCACTCAA	TTGAGTGCGGTACTTGCAGCGATG

TABLE 4

Seq. ID No.	Decoder Sequence (5'-3') + 5' T	Probe Sequence (5'-3') + 5' T
17	TTTCGCCGTCGTGTAGGCTTTTCAA	TTTGAAAAGCCTACACGACGGCGAA
18	TGTTCCCAGTGAAGCTGCGATCTGG	TCCAGATCGCAGCTTCACTGGGAAC
19	TTACTTGGCATGGAATCCCTTACGC	TGCGTAAGGGATTCCATGCCAAGTA
20	TACTAGCATATTTCAGGGCACCGGC	TGCCGGTGCCCTGAAATATGCTAGT
21	TGAACGGTCAATGAACCCGCTGTGA	TTCACAGCGGGTTCATTGACCGTTC
22	TGCGGCCTTGGTTCAATATGAATCG	TCGATTCATATTGAACCAAGGCCGC
23	TGATCGTTAGAGGGACCTTGCCCGA	TTCGGGCAAGGTCCCTCTAACGATC
24	TTGGACCTAGTCCGGCAGTGACGAA	TTTCGTCACTGCCGGACTAGGTCCA
25	TATAAACTACCCAGGACGGGCGGAA	TTTCCGCCCGTCCTGGGTAGTTTAT
26	TCATCGGTTCGCGCCAATCCAGATA	TTATCTGGATTGGCGCGAACCGATG
27	TGTCGGGCATAGAGCCGACCACCCT	TAGGGTGGTCGGCTCTATGCCCGAC
28	TCTTGGGTCATGATTCACCGTGCTA	TTAGCACGGTGAATCATGACCCAAG
29	TTGCCTAACGTGCTAATCAGCAGCG	TCGCTGCTGATTAGCACGTTAGGCA
30	TCGCATGTTGGAGCATATGCCCTGA	TTCAGGGCATATGCTCCAACATGCG
31	TAGCCACTGCATCAGTGCTGTTCAA	TTTGAACAGCACTGATGCAGTGGCT
32	TGGTTGTTTTGAGGCGTCCCACACT	TAGTGTGGGACGCCTCAAAACAACC
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35	TGAAATACGAAGTCTGCGGGAGTCG	TCGACTCCCGCAGACTTCGTATTTC
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37	TATATCGGGATTCGTTCCCGGTGAA	TTTCACCGGGAACGAATCCCGATAT
38	TGCGAGCGTACCGAAGGGCCTAGAA	TTTCTAGGCCCTTCGGTACGCTCGC
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41	TCCTGTTAGCGTAGGCGAGTCGATC	TGATCGACTCGCCTACGCTAACAGG
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43	TGGTACATGCACTACGCGCACTCGG	TCCGAGTGCGCGTAGTGCATGTACC
44	TAATTCATCTCGGACTCCCGCGGTA	TTACCGCGGGAGTCCGAGATGAATT
45	TGCCAAATCTGGATTGGCAGGAATG	TCATTCCTGCCAATCCAGATTTGGC
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47	TCCGCTCAATTCACCATGCTTCGCT	TAGCGAAGCATGGTGAATTGAGCGG
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49	TAATTCGACCAGCAGAACGTCCCAT	TATGGGACGTTCTGCTGGTCGAATT
50	TGCCAGAGTCTCAACCTCACGGGAT	TATCCCGTGAGGTTGAGACTCTGGC
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52	TGAGAACTGATCGCTGAGGGGCATG	TCATGCCCCTCAGCGATCAGTTCTC
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57	TGTTGGTATCTATGGCAGAGGCGGA	TTCCGCCTCTGCCATAGATACCAAC
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61	TTGATGAGCCTCAGGGTACGAGGCA	TTGCCTCGTACCCTGAGGCTCATCA
62	TCACCGCGGTGTTCCTACAGAATGA	TTCATTCTGTAGGAACACCGCGGTG
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315	TAGACAGCGATCCGCGGCTCATGAT	TATCATGAGCCGCGGATCGCTGTCT
316	TCGCGTCTCTAACTGAGAGCAGCCA	TTGGCTGCTCTCAGTTAGAGACGCG
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319	TTGATCCATATTGTCGGACGTTGCG	TCGCAACGTCCGACAATATGGATCA
320	TACCTGCCGGGAGTTCATAGGCTAG	TCTAGCCTATGAACTCCCGGCAGGT
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323	TATAGCGTACGACGAGGTGACGCGC	TGCGCGTCACCTCGTCGTACGCTAT
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326	TCCTTTGGCCTGAAGTTGTCGTAGC	TGCTACGACAACTTCAGGCCAAAGG
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338	TGAGCTTAGTTTGCGGTCATCGGGC	TGCCCGATGACCGCAAACTAAGCTC
339	TTGTTTGCCGCCATTAGGGAGTAAC	TGTTACTCCCTAATGGCGGCAAACA
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596	TCGGTCTCAGCAACACTGTCGCAAA	TTTTGCGACAGTGTTGCTGAGACCG
597	TCGAACGTTCTCCGATGTAATGGCC	TGGCCATTACATCGGAGAACGTTCG
598	TATACCGTGCGACAAGCCCCTCTGA	TTCAGAGGGGCTTGTCGCACGGTAT
599	TAGCTCATTCCCGAGACGGAACACC	TGGTGTTCCGTCTCGGGAATGAGCT
600	TTTTCATGCGGCCGTTGCAAATCAT	TATGATTTGCAACGGCCGCATGAAA
601	TACTCGAACGGACGTTCAATTCCCA	TTGGGAATTGAACGTCCGTTCGAGT
602	TCTGCATGGTGTGGGTGAGACTCCC	TGGGAGTCTCACCCACACCATGCAG
603	TCCGCGAGTGTGGATGGCGTGTTGA	TTCAACACGCCATCCACACTCGCGG
604	TAATGTGTCGGTCCTAAGCCGGGTG	TCACCCGGCTTAGGACCGACACATT
605	TTAAGACGAGCCTGCACAGCTTGCG	TCGCAAGCTGTGCAGGCTCGTCTTA
606	TGGCGTGGGAGGATAAGACGATGTC	TGACATCGTCTTATCCTCCCACGCC
607	TTGCTCCATGTTAGGAACGCACCAC	TGTGGTGCGTTCCTAACATGGAGCA
608	TCGGTGTTGGTCGGACTGACGACTG	TCAGTCGTCAGTCCGACCAACACCG
609	TCCGCGCGTATCTATCAGATCTGGG	TCCCAGATCTGATAGATACGCGCGG
610	TAAAGCATGCTCCACCTGGAGCGAG	TCTCGCTCCAGGTGGAGCATGCTTT
611	TACTTGCATCGCTGGGTAGATCCGG	TCCGGATCTACCCAGCGATGCAAGT
612	TTGCTTACGCAGTGGATTGGTCAGA	TTCTGACCAATCCACTGCGTAAGCA
613	TATGCAGATGAACAAATCGCCGAAT	TATTCGGCGATTTGTTCATCTGCAT
614	TGCAATTCTGGGCCATGTATTCGTC	TGACGAATACATGGCCCAGAATTGC
615	TAGGGTTCCTTACGCGTCGACATGG	TCCATGTCGACGCGTAAGGAACCCT
616	TGTGGAGCTAATCGCGAGCCTCAGA	TTCTGAGGCTCGCGATTAGCTCCAC
617	TTCGTAGTCTCACCGGCAATGATCC	TGGATCATTGCCGGTGAGACTACGA
618	TTTATAGCAGTGCGCCAATGCTTCG	TCGAAGCATTGGCGCACTGCTATAA
619	TCGAACAGTGCTGTCCGTCGCTCAA	TTTGAGCGACGGACAGCACTGTTCG
620	TTCCGCGTGGACTGTTAGACGCTAT	TATAGCGTCTAACAGTCCACGCGGA
621	TCATTAGCCCGCTGTCGGTAACTGT	TACAGTTACCGACAGCGGGCTAATG
622	TGGAAAGAAACTCAGACGCGCAATG	TCATTGCGCGTCTGAGTTTCTTTCC
623	TCGACTCGCTGGACAGGAGAATCGT	TACGATTCTCCTGTCCAGCGAGTCG
624	TCATGATCCTCTGTTTCACCCGCGG	TCCGCGGGTGAAACAGAGGATCATG
625	TGGCGTAGCGCTCTAAAAGCTTCGG	TCCGAAGCTTTTAGAGCGCTACGCC
626	TAGTGATGCCATCAGGCCCGTATAC	TGTATACGGGCCTGATGGCATCACT
627	TTATGGAAAGGGCAACAGCGCTATC	TGATAGCGCTGTTGCCCTTTCCATA

628	TCTGTGGTTGATGGAGGATCCACAC	TGTGTGGATCCTCCATCAACCACAG
629	TACTCGCTGGAATTTGCGCTGACAC	TGTGTCAGCGCAAATTCCAGCGAGT
630	TCAGGCCCGAACCACGCGGTTACAG	TCTGTAACCGCGTGGTTCGGGCCTG
631	TGGCGCAATGGGCGCATAAATACTA	TTAGTATTTATGCGCCCATTGCGCC
632	TGGTCAATTCGCGCTACATGCCCTA	TTAGGGCATGTAGCGCGAATTGACC
633	TGATGGTGGACTGGAGCCCTTCCGC	TGCGGAAGGGCTCCAGTCCACCATC
634	TCCGCGCATAGCGCAATAGGGGAGA	TTCTCCCCTATTGCGCTATGCGCGG
635	TTCTTCTGGCTGTCCGGCACCCGAA	TTTCGGGTGCCGGACAGCCAGAAGA
636	TGCGTTCGCAATTCACGGGCCCTTA	TTAAGGGCCCGTGAATTGCGAACGC
637	TTCGTTTCGGCCTTGGAGAGTATCG	TCGATACTCTCCAAGGCCGAAACGA
638	TAGGTGCAAGTGCAAGGCGAGAGGC	TGCCTCTCGCCTTGCACTTGCACCT
639	TCGCCAGTTTCGATGGCTGACGTTT	TAAACGTCAGCCATCGAAACTGGCG
640	TGCTTTACCGCCGATCCCAGATATC	TGATATCTGGGATCGGCGGTAAAGC
641	TGTGCTTGACGAAGAGGCGAAATGT	TACATTTCGCCTCTTCGTCAAGCAC
642	TCAGTCCGTGCGCTTCATGTCCTCA	TTGAGGACATGAAGCGCACGGACTG
643	TTACGCGTAAGAGCCTACCCTCGCG	TCGCGAGGGTAGGCTCTTACGCGTA
644	TGGCGAGTCTTGTGGGGACATGTGT	TACACATGTCCCCACAAGACTCGCC
645	TCCAAAGCGAAGCGAGCGTGTCTAT	TATAGACACGCTCGCTTCGCTTTGG
646	TGCCGTAGGTTGCTCTTCACCGAAC	TGTTCGGTGAAGAGCAACCTACGGC
647	TAAATCCGCGATGTGCCGTGAGGCT	TAGCCTCACGGCACATCGCGGATTT
648	TGGCTTCGCACCCGTACCAATTTAG	TCTAAATTGGTACGGGTGCGAAGCC
649	TTGTAGAGTCCCACGTAGCCGGCAT	TATGCCGGCTACGTGGGACTCTACA
650	TCACTAGTCTGGGGCAAGGTGCATT	TAATGCACCTTGCCCCAGACTAGTG
651	TTGTACTCGGCAGGCGCAATAGATT	TAATCTATTGCGCCTGCCGAGTACA
652	TAACGGGTATCGGAAGCGTAAAAGC	TGCTTTTACGCTTCCGATACCCGTT
653	TCGGACTGCCCGTTTGCAAGTTGAG	TCTCAACTTGCAAACGGGCAGTCCG
654	TATCGTTCAGCACTGGAGCCCGTAA	TTTACGGGCTCCAGTGCTGAACGAT
655	TATGCATCGAACTAGTCGTGACGGC	TGCCGTCACGACTAGTTCGATGCAT
656	TTTCCAGGCATTAAGGAGAGGGAGC	TGCTCCCTCTCCTTAATGCCTGGAA
657	TGTGCGACATCTACTCCACGATCCC	TGGGATCGTGGAGTAGATGTCGCAC
658	TCTCATCGTCCTAACACGAGAGCCC	TGGGCTCTCGTGTTAGGACGATGAG
659	TAATGGCACTTCGGCGGTGATGCAA	TTTGCATCACCGCCGAAGTGCCATT
660	TCCGTGGGAGGGAATCCAACCGAGG	TCCTCGGTTGGATTCCCTCCCACGG
661	TAAATTCTCGTTGGTGACGGCTCAT	TATGAGCCGTCACCAACGAGAATTT
662	TTTGCTCTTATCCTTGTCCTGGGCG	TCGCCCAGGACAAGGATAAGAGCAA
663	TTTAAGGATCAGGCGGAGCTTGCAG	TCTGCAAGCTCCGCCTGATCCTTAA
664	TCGCGACTAAGGTGCTGCAACTCGA	TTCGAGTTGCAGCACCTTAGTCGCG
665	TGCTCGATTTCACGGCCCGTTGTTC	TGAACAACGGGCCGTGAAATCGAGC
666	TAGCAGAGTGCGTTGCAGAGGCTAA	TTTAGCCTCTGCAACGCACTCTGCT
667	TTGGAGGTGAGGACGACGTGCACTA	TTAGTGCACGTCGTCCTCACCTCCA
668	TAACCGTTTAGGGTACATTCGCGGT	TACCGCGAATGTACCCTAAACGGTT

669	TTATGATCGCTCGGCTCACAGTTTG	TCAAACTGTGAGCCGAGCGATCATA
670	TGACTTTTTGCGGAAACGTCATGGT	TACCATGACGTTTCCGCAAAAAGTC
671	TTGTCGGTTATTCCACCTGCAAGGA	TTCCTTGCAGGTGGAATAACCGACA
672	TCTATGGTTTGCACTGCGCCGTCGA	TTCGACGGCGCAGTGCAAACCATAG
673	TAGCAGGGAAATTCAATCGTTCGCA	TTGCGAACGATTGAATTTCCCTGCT
674	TCCTAACCGAGCGCTTAGCATTTCC	TGGAAATGCTAAGCGCTCGGTTAGG
675	TCCCGACCCTAACTCGCATTGAATA	TTATTCAATGCGAGTTAGGGTCGGG
676	TTTGCTTAATGGTGACGCCACGGAT	TATCCGTGGCGTCACCATTAAGCAA
677	TGATGCTCGCCGTGTTTAGTTCACG	TCGTGAACTAAACACGGCGAGCATC
678	TTCGGATGACGAGTTTCCATGACGG	TCCGTCATGGAAACTCGTCATCCGA
679	TATGCGGTCTACTTTCTCGATCGGG	TCCCGATCGAGAAAGTAGACCGCAT
680	TTTGCGAGGCTAAGCACACGGTAAA	TTTTACCGTGTGCTTAGCCTCGCAA
681	TAACTTAATTACCGCCTCTGGCGCC	TGGCGCCAGAGGCGGTAATTAAGTT
682	TGTGACCGCGAACTTGTTCCGACAG	TCTGTCGGAACAAGTTCGCGGTCAC
683	TTGCGGATTACCGATTCGCTCTTAA	TTTAAGAGCGAATCGGTAATCCGCA
684	TTGATAGGGGGCCACGTTGATCAGA	TTCTGATCAACGTGGCCCCCTATCA
685	TTCGCTCCGTAGCGATTCATCGTAG	TCTACGATGAATCGCTACGGAGCGA
686	TTGTCAGCTGGTAGCCTCCGTTTGA	TTCAAACGGAGGCTACCAGCTGACA
687	TAGCGTCGCATGACGCTTACGGCAC	TGTGCCGTAAGCGTCATGCGACGCT
14	TAGACGCACCGCAACAGGCTGTCAA	TTTGACAGCCTGTTGCGGTGCGTCT
15	TCGTGTAGGGGTCCCGTGCTGTCAA	TTTGACAGCACGGGACCCCTACACG
690	TGTCGCATTCTGCACTGGCTTCGCC	TGGCGAAGCCAGTGCAGAATGCGAC
691	TTGATTAGGTGCGGTCCCGTAGTCC	TGGACTACGGGACCGCACCTAATCA
692	TAAGGGACCTTGGGTGACGGCGAGA	TTCTCGCCGTCACCCAAGGTCCCTT
693	TTCAAATGGCCACCGCGTGTCATTC	TGAATGACACGCGGTGGCCATTTGA
694	TCTCCGACGACCAATAAATAGCCGC	TGCGGCTATTTATTGGTCGTCGGAG
695	TGGCTATTCCCGTAGAGAGCGTCCA	TTGGACGCTCTCTACGGGAATAGCC
696	TTGGATAACCTCTCGGTCCATCCAC	TGTGGATGGACCGAGAGGTTATCCA
697	TGACCGCTGTACGGGAGTGTGCCTT	TAAGGCACACTCCCGTACAGCGGTC
698	TGCCACAGAGTTTTAGCAGGGACCC	TGGGTCCCTGCTAAAACTCTGTGGC
699	TCCCACGCTTTCCGACCACTGACCT	TAGGTCAGTGGTCGGAAAGCGTGGG
700	TCATTGACACAATGCGGGGACTGAT	TATCAGTCCCCGCATTGTGTCAATG
701	TAGCCACTCGACAGGGTTCCAAAGC	TGCTTTGGAACCCTGTCGAGTGGCT
702	TCAGGATGAGCAAAGCGACTCTCCA	TTGGAGAGTCGCTTTGCTCATCCTG
703	TCAAGGTATGGTCTGGGGCCTAAGC	TGCTTAGGCCCCAGACCATACCTTG
704	TGGTGTTCGGCCTAAACTCTTTCGG	TCCGAAAGAGTTTAGGCCGAACACC
705	TTTTAGTCGGACCCTGTGGCAATTC	TGAATTGCCACAGGGTCCGACTAAA
706	TCACACGTTTCCGACCAGCCTGAAC	TGTTCAGGCTGGTCGGAAACGTGTG
707	TCTGGACGAACTGGCTTCCTCGTAC	TGTACGAGGAAGCCAGTTCGTCCAG
708	TTTCACAATCCGCCGAAAACTGACC	TGGTCAGTTTTCGGCGGATTGTGAA
709	TAACAGGATATCCGCGATCACGACA	TTGTCGTGATCGCGGATATCCTGTT

710	TTACGTCGGATCCATTGCGCCGAGT	TACTCGGCGCAATGGATCCGACGTA
711	TCATGGATCTCTCGGTTTGATCGCC	TGGCGATCAAACCGAGAGATCCATG
712	TAGCCAGGCGCGTATATACGCTCGG	TCCGAGCGTATATACGCGCCTGGCT
713	TATTTGGCACGTGTCGTGCCATGTT	TAACATGGCACGACACGTGCCAAAT
714	TCCGCGTTGCACCACTTTGAGGTGC	TGCACCTCAAAGTGGTGCAACGCGG
715	TTTGGACGTGACAAGCATGGCGCTC	TGAGCGCCATGCTTGTCACGTCCAA
716	TCTGAATCGCGCAAGTAAATGGGGG	TCCCCCATTTACTTGCGCGATTCAG
717	TGATAAGGTCCACCAGATTGCGCGC	TGCGCGCAATCTGGTGGACCTTATC
718	TCTAACAATTGCCAACCGGGACGGC	TGCCGTCCCGGTTGGCAATTGTTAG
719	TGGTAACCTGGGTGCTTGCAGGTTA	TTAACCTGCAAGCACCCAGGTTACC
720	TATCGGAGCCACCATTCGCATTGGG	TCCCAATGCGAATGGTGGCTCCGAT
721	TGTGAACTGGCTTGCCCCAGGATTA	TTAATCCTGGGGCAAGCCAGTTCAC
722	TAGGCGATAGCATGGTCCCATATGA	TTCATATGGGACCATGCTATCGCCT
723	TAACGGTATCGTGGCTAATGCACGA	TTCGTGCATTAGCCACGATACCGTT
724	TAGTAGTGGTCCTCCAGATCGGCAA	TTTGCCGATCTGGAGGACCACTACT
725	TCCGTTGAATTGGACGGGAGGTTAG	TCTAACCTCCCGTCCAATTCAACGG
726	TGCATAAGTGCGGCATCGCGAAGGG	TCCCTTCGCGATGCCGCACTTATGC
727	TCGACAAGATGCAGCTGCTACATGC	TGCATGTAGCAGCTGCATCTTGTCG
728	TTCGCAGTGATTCCCGACCGATAAG	TCTTATCGGTCGGGAATCACTGCGA
729	TCAAGGCGAGTCCACTCGAGGGGAC	TGTCCCCTCGAGTGGACTCGCCTTG
730	TGCAACTTGCACGGCATAAGTGGCC	TGGCCACTTATGCCGTGCAAGTTGC
731	TTCCGAGCTTGACGTTCGCGACGTC	TGACGTCGCGAACGTCAAGCTCGGA
732	TAGCGCTGGGCTGTGCTGCCATCTC	TGAGATGGCAGCACAGCCCAGCGCT
733	TTTCATGTCGCTGAGTAACCCTCGC	TGCGAGGGTTACTCAGCGACATGAA
734	TCGAACCGCTAATGCCCATTGTCAG	TCTGACAATGGGCATTAGCGGTTCG
735	TCACGGAAGGTGGGACAAATCGCCG	TCGGCGATTTGTCCCACCTTCCGTG
736	TCACAGATGGAGACAAACGCGCCTT	TAAGGCGCGTTTGTCTCCATCTGTG
737	TTTTTCGCAACTCGCTCCATAACCC	TGGGTTATGGAGCGAGTTGCGAAAA
738	TACGTTACGTTTCCGGCGCCTCTAA	TTTAGAGGCGCCGGAAACGTAACGT
739	TTATCGGATTGCGTGGGTTTCAATC	TGATTGAAACCCACGCAATCCGATA
740	TCTTCCACAATTGTCTGCGACGCAC	TGTGCGTCGCAGACAATTGTGGAAG
741	TTGCACAAAGGTATGGCTGTCCGGC	TGCCGGACAGCCATACCTTTGTGCA
742	TTCCGATGCCAGTCCCATCTTAAGA	TTCTTAAGATGGGACTGGCATCGGA
743	TCTGAAACCGTGCGAATCGAGGTGA	TTCACCTCGATTCGCACGGTTTCAG
744	TCGGTGTTCCGCGTGTCGAAAAAAT	TATTTTTTCGACACGCGGAACACCG
745	TTCTAGCAGGCCTTTTGAATCGCCA	TTGGCGATTCAAAAGGCCTGCTAGA
746	TGAGTCACCTCTGAGACGGACGCCA	TTGGCGTCCGTCTCAGAGGTGACTC
747	TTCTTCTGTCATCCTGCAGCAGCAT	TATGCTGCTGCAGGATGACAGAAGA
748	TGCGGATGAAACCTGAAAGGGGCCT	TAGGCCCCTTTCAGGTTTCATCCGC
749	TGGGGCCCCAAACTGGTATCAAGCC	TGGCTTGATACCAGTTTGGGGCCCC
750	TGCATTGGCTTCGGATTCTCCTACA	TTGTAGGAGAATCCGAAGCCAATGC

751	TAGGCGGCCCAACTGTGAGGTCTTG	TCAAGACCTCACAGTTGGGCCGCCT
752	TACACCATGTGCTCCGCGCTGCAGT	TACTGCAGCGCGGAGCACATGGTGT
753	TACGATGAACATGAATCGGGAGTCG	TCGACTCCCGATTCATGTTCATCGT
754	TCTGCATCCCTGTAGCAGCGCTCCG	TCGGAGCGCTGCTACAGGGATGCAG
755	TGTGCCGTATTTCGACCTGTGCGTT	TAACGCACAGGTCGAAATACGGCAC
756	TGCAGTGCGCACTTCAGTTCAAAAG	TCTTTTGAACTGAAGTGCGCACTGC
757	TGCGATTTTAAGCGATGCCTTGACG	TCGTCAAGGCATCGCTTAAAATCGC
758	TTAGGTGACCTAGGCTTGCTTGCGG	TCCGCAAGCAAGCCTAGGTCACCTA
759	TCTGGATACCTTGCCTGTGCGGCGC	TGCGCCGCACAGGCAAGGTATCCAG
760	TCCCCTTACGGCTCGTCGTCTATGC	TGCATAGACGACGAGCCGTAAGGGG
761	TGCGCTTGCCCGATGCGATGCATTA	TTAATGCATCGCATCGGGCAAGCGC
762	TTTTCTGTAAGCGGCCTGGGGTTCA	TTGAACCCCAGGCCGCTTACAGAAA
763	TGGCTGAGGTGAGCGGTAAGGATGA	TTCATCCTTACCGCTCACCTCAGCC
764	TTCTTGGCCTCCCCGATCTAATTTG	TCAAATTAGATCGGGGAGGCCAAGA
765	TGGAGGTAACGCCGTGTACGTAGGA	TTCCTACGTACACGGCGTTACCTCC
766	TGTAATCCATTTGTGGCTGCGTCAA	TTTGACGCAGCCACAAATGGATTAC
767	TCAAACCCATTCCAGCAGACGCCTG	TCAGGCGTCTGCTGGAATGGGTTTG
768	TTAGGAGGAATTTGGCATGCGGGCG	TCGCCCGCATGCCAAATTCCTCCTA
769	TATAGGTAGGATGTGCCCGGCGTTG	TCAACGCCGGGCACATCCTACCTAT
770	TGCAAGTGCTTAGCTCGTCAGCCTC	TGAGGCTGACGAGCTAAGCACTTGC
771	TCTGGCTGTGTCGCATCTCGTTAAC	TGTTAACGAGATGCGACACAGCCAG
772	TCTAACGTCGTCTCGCGCAATCACT	TAGTGATTGCGCGAGACGACGTTAG
773	TTTTTCATAAACGTTGTCCCCGAGC	TGCTCGGGGACAACGTTTATGAAAA
774	TAGCAGGAGGACGAACCTCCGCTCC	TGGAGCGGAGGTTCGTCCTCCTGCT
775	TTTCAAGCACCATCGTGCAATCCAA	TTTGGATTGCACGATGGTGCTTGAA
776	TAGCGTCGCCAGTGATCGCTAGTGG	TCCACTAGCGATCACTGGCGACGCT
777	TTACATTCCCTGCCTCCGTGGGCTT	TAAGCCCACGGAGGCAGGGAATGTA
778	TCGCTTCGCGTATTCAGTAGCGGTT	TAACCGCTACTGAATACGCGAAGCG
779	TTCGGACGCGTCGACACTCATTATA	TTATAATGAGTGTCGACGCGTCCGA
780	TTCTGAGCAGGCCAGCGCTCCAGCT	TAGCTGGAGCGCTGGCCTGCTCAGA
781	TTTGAATTGCCAAGCCCTGAAAGCC	TGGCTTTCAGGGCTTGGCAATTCAA
782	TAGTTTTCGCCTTGATGCGTCGGTG	TCACCGACGCATCAAGGCGAAAACT
783	TGTTTCATAGGCCACGCGTGCTAAA	TTTTAGCACGCGTGGCCTATGAAAC
16	TCATCGCTGCAAGTACCGCACTCAA	TTTGAGTGCGGTACTTGCAGCGATG

CLAIMS

We claim:

1. An oligonucleotide array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

2. An array according to claim 1, wherein said capture probes are microspheres.

3. An array according to claim 1 or 2 wherein said array is a liquid array.

4. An array according to claim 1, 2 or 3, wherein said array further comprises a solid support.

5. An array according to claim 1, 2, 3 or 4, wherein said addresses are microspheres and wherein said solid support comprises wells into which said microspheres are individually distributed.

6. An array according to claim 1, 2, 3 or 4, wherein each address is a different known location, and said wherein each capture probe is attached to one of said known locations.

7. An array according to claim 1, 2, 3, 4, 5 or 6, wherein said array comprises at least 50 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

8. An array according to claim 1,2, 3, 4, 5 or 6 wherein said array comprises at least 100 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.

9. A kit comprising at least twenty-five nucleic acids selected from the group consisting of sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

10. A kit according to claim 9, wherein said kit comprises at least 50 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

11. A kit according to claim 9 or 10, wherein said kit comprises at least 100 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.

12. A kit according to claim 9, 10 or 11, wherein said nucleic acids further comprise at least a first universal priming sequence.

13. A kit according to claim 9, 10, 11 or 12, wherein said nucleic acid sequence further comprises a sequence substantially complementary to a target domain.

14. A method of immobilizing a target nucleic acid sequence, said method comprising:
a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;
b) contacting said modified first target nucleic acid sequence with an array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4, whereby said target nucleic acid sequence is immobilized.

15. A method of detecting a target nucleic acid sequence, said method comprising:
a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;
b) contacting said modified first target nucleic acid sequence with an array comprising: an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4; and
c) detecting the presence of said modified first target nucleic acid sequence.

16. A method of detecting a target nucleic acid, said method comprising:
   a) hybridizing a first adapter probe with a first target nucleic acid, said first adapter probe comprising a first domain that is complementary to said first target nucleic acid and a second domain, said second domain comprising a first sequence substantially complementary to a selected from the group consisting of the sequences set forth in Table I, Table II, Table III and Table IV to form a first hybridization complex;

b) contacting said first hybridization complex with an enzyme such that when said first domain of said adapter probe is perfectly complementary with said first target nucleic acid, said first adapter probe is altered resulting in a modified first adapter probe;

c) contacting said modified first adapter probe with a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that said first capture probe and said modified first adapter probe form a second hybridization complex; and

d) detecting the presence of said modified first adapter probe as an indication of the presence of said target nucleic acid.

Description of algorithm to select "best" oligonucleotide adapter sequences.

Requirements for good sequences:

- Generates adequate hybridization signal intensity when employed in an experiment.
- Exhibits minimal cross-reactivity with other adapter sequences.
- Unique within the human genome sequence. This requirement can be extended to the genomic sequence of other organisms such as the fruit fly, the mouse, etc.

One method of generating sequences that meet the above requirements is to randomly generate sequences of given lengths and then pass these filters through a set of heuristic acceptance filters. In particular, the 24-mer Illumina Adapter sequences (IllumaCodes) were chosen as follows.

Generate a Random 24-mer Oligonucleotide Sequence	Computer randomly picks sequences from space of 24-mer oligonucleotide sequences.
↓ $Abs(T_m - T_{thres}) < 5$ ^C Where $T_{thres} = 72$ ^C	Oligo Tm must be within a define range. This requirement increases uniformity of hybridization signal.
↓ $Abs(GG_{Content} - GC_{thres}) < 0.15$	GC content must be balanced with AT content of oligo. This reduces sequence specific effects of hybridization.
↓ Self-Complementary Score < 14	Reduces oligonucleotide hairpin structures.
↓ $GC_{run} < 5$	A run of Gs or Cs can lead to poorly hybridizing probes through G quartet structures.
↓ Decoder-Decoder Complementarity Score < 18	A high decoder-decoder complementarity score indicates that the two decoders are likely to cross-hybridize in solution.
↓ Probe-Decoder Complementarity Score < 14	A high probe-decoder complementarity score indicates that the decoder is likely to cross-hybridize with the probe.
↓ Blast Against Genome Databases (Unigene DB)	The generated sequences are screened against a specified genomic database.

FIG._1

Flow diagram for selection of probes sequences

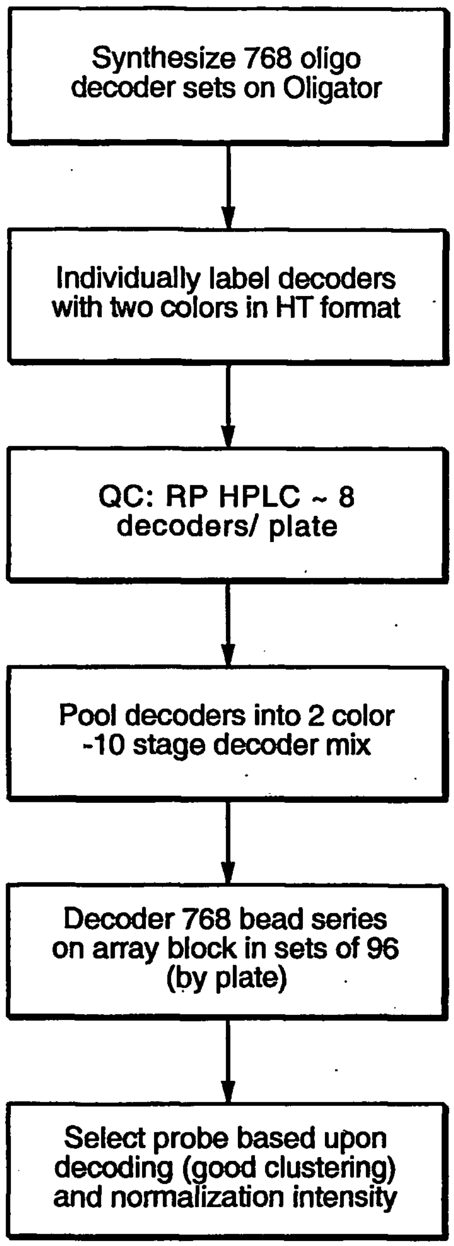

FIG._2

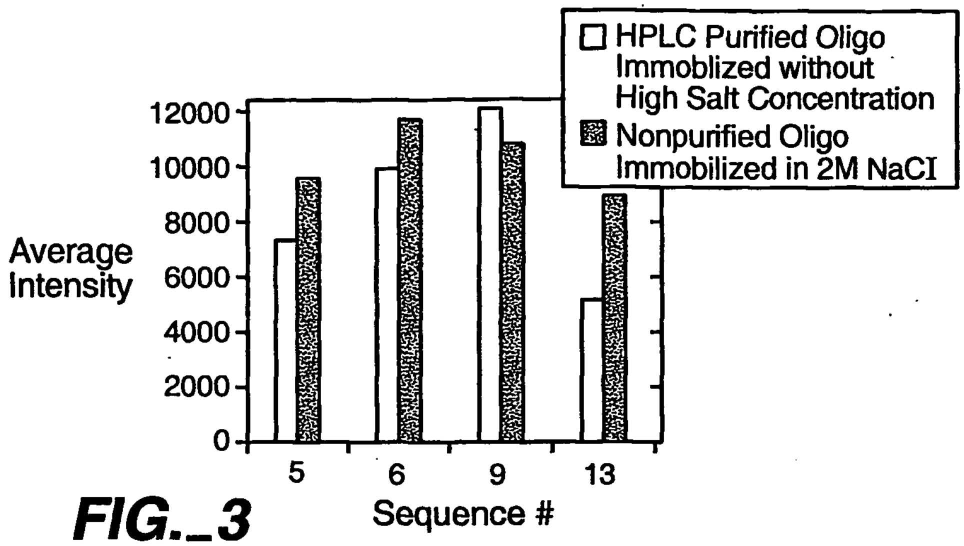

FIG._3

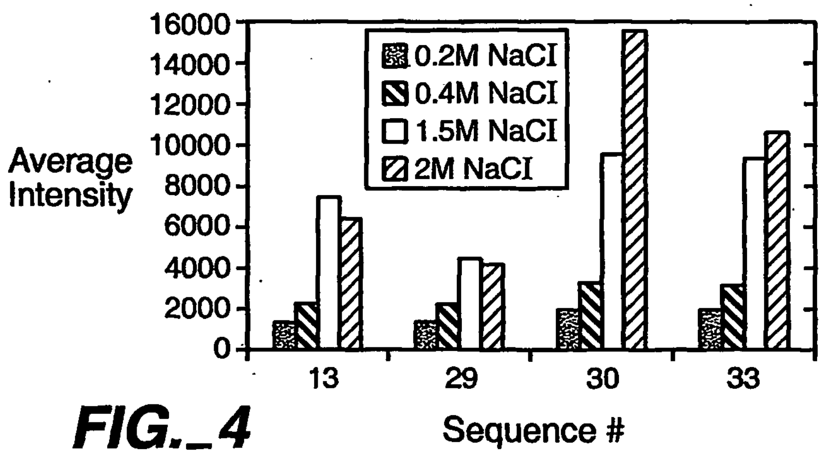

FIG._4

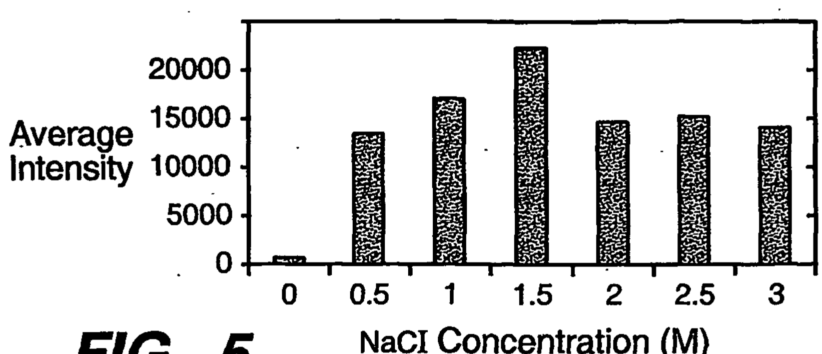

FIG._5